

STIC-Biotech/ChemLib

142759

CRFE

From: Ramirez, Delia
Sent: Tuesday, January 18, 2005 1:06 PM
To: STIC-Biotech/ChemLib
Subject: case 09/459,573

Hi,

I would like to request the following interference search: SEQ ID NO:10 in the protein and nucleic acid databases.

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____
Searcher: Beverly e 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 16:33:23 ; Search time 40 Seconds
(without alignments)
369.723 Million cell updates/sec

Title: US-09-459-573-10
Perfect score: 1135
Sequence: 1 MMQLVHLFMDEITMDPLHAV.....IGAIIGVFALRLIYEGVTQR 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		Issued Patents AA:**	
1:	/cgn2_6/ptodata/1/iaa/5A COMB.pap:**		
2:	/cgn2_6/ptodata/1/iaa/5B COMB.pap:**		
3:	/cgn2_6/ptodata/1/iaa/6A COMB.pap:**		
4:	/cgn2_6/ptodata/1/iaa/6B COMB.pap:**		
5:	/cgn2_6/ptodata/1/iaa/PCUS COMB.pap:**		
6:	/cgn2_6/ptodata/1/iaa/backfiles1.pap:**		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	270	23.8	217	4	US-09-489-039A-8076
2	260	22.9	249	4	US-09-328-352-5813
3	245.5	21.6	269	4	US-09-489-039A-7130
4	237.5	20.9	214	4	US-09-328-352-6695
5	226	19.9	216	4	US-09-252-991A-18666
6	224	19.7	219	4	US-09-489-039A-7731
7	221	19.5	226	4	US-09-252-991A-31610
8	220.5	19.4	215	4	US-09-328-352-4775
9	220.5	19.4	215	4	US-09-328-352-8249
10	207	18.2	260	4	US-09-252-991A-25992
11	190.5	16.8	231	4	US-09-489-039A-8849
12	186	16.4	206	4	US-09-543-681A-4854
13	182	16.0	208	4	US-09-328-352-4784
14	179	15.8	210	4	US-09-710-479-708
15	179	15.8	224	3	US-09-134-001C-4608
16	176	15.5	237	4	US-09-252-991A-27175
17	176	15.5	211	4	US-09-489-039A-9608
18	173.5	15.3	214	4	US-09-489-039A-9793
19	167	14.7	214	4	US-09-252-991A-23837
20	166.5	14.7	228	4	US-09-328-352-7159
21	165	14.5	241	4	US-09-328-352-7159
22	164	14.4	222	4	US-09-252-991A-16947
23	156.5	13.8	213	4	US-09-252-991A-16947
24	150.5	13.3	214	4	US-09-543-681A-4972
25	144.5	12.7	250	4	US-09-543-681A-4487
26	143	12.6	277	4	US-09-252-991A-23018
27	139	12.2	213	4	US-09-489-039A-11845

ALIGNMENTS

RESULT 1
US-09-489-039A-8076
; Sequence 8076, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8076
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8076

Query Match		23.8%; Score 270; DB 4; Length 217;	
Best Local Similarity		28.8%; Pred. No. 6.3e-22;	
Matches		64; Conservative 51; Mismatches 89; Indels 18; Gaps 4;	
QY	4	LVLHLMDEITMDPLHAVLYLVGL-FVITFPNPGANL FVVVOTSLASGRAGVLTGLGVAL	62
DB	2	LSSLFSCETLMLL---FLTVLHVHIIALMSFGPDFFVSQTATSRSRREMMGVLTIC	58
QY	63	GDIFYSGLGFLGLATLITQCBEIFSLIRIVGGAYLWFAWCSMR-----ROSTPQMS	114
DB	59	GVWVWAGVALLGLNLILARMAWLHNIIMVGGGLYLCMMGYQMLRGALKKKTVASAEQVE	118
QY	115	TLQOPISAPWYFFRRGITDLSNPQTVLFFISIFSVTLNAETPTWAPLMAWAGIVLASI	174
DB	119	LARSGRS-----FVKGLLTNLNPKAIYFGSVFSLFVGDVSGAGARWGFLLIIVETL	172
QY	175	IWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAILGVFALRLI	216
DB	173	AWFMVASLIFALPGMRGVRQMAKWDIAGTTLFAGFGIHLI	214

RESULT 2
US-09-328-352-5813
; Sequence 5813, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA


```
Db 135 PKTCLFVVSLFMQVIDPHTALPAQLGCGAFIALAHVAMFGLVACFLSSPAVNRGLLRFR 194
Qy 199 VASRVIGAIIGVFALRL 215
Db 195 RIDQFFGALLVFGVLL 211

RESULT 6
US-09-489-039A-7731
; Sequence 7731, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1432
; SEQ ID NO 7731
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7731

Query Match 19.7%; Score 224; DB 4; Length 219;
Best Local Similarity 30.7%; Pred. No. 8.1e-17;
Matches 63; Conservative 39; Mismatches 89; Indels 14; Gaps 6;

Qy 18 HAVLTGVLFTFFNCGANLFFVVTSLASGRAGVLTGLGVALGDAFYSGLGFL 77
Db 17 YLTGVLGAVFLLV--PGNFFVFKIGIAHGKGYLAAGVFIGDAVLMFLAFAGVAT 74

Qy 78 LITQCEIEISLRIVGGAYLLWFA---WCSMRQSTPQMSLTQOPIAPWVFFRGLIT 134
Db 75 LITQCEIEISLRIVGGAYLLWFA---WCSMRQSTPQMSLTQOPIAPWVFFRGLIT 130

Qy 135 DLNPOTVLFFISIF--SVTLNAETPTWRLMAWAGIVLASIIRVVF--LSQAFSLPAVR 190
Db 131 SLNPKIAVLVSVFVQVQIDVNAKTPGVAFVILALTLEIVSFYMSFLILSGSFVTRYV- 189

Qy 191 RAYGRMORVASRVIGAIIGVFALRL 215
Db 190 KTRKRLAKLGNLSLGLVFGVFAARL 214

RESULT 7
US-09-252-991A-31610
; Sequence 31610, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31610
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31610

Query Match 19.5%; Score 221; DB 4; Length 226;
Best Local Similarity 27.2%; Pred. No. 1.8e-16;
Matches 55; Conservative 46; Mismatches 85; Indels 16; Gaps 6;
```

```
Qy 18 HAVYLTGVLFTVIT-----FENCGANLFFVVTSLASGRAGVLTGLGVALGDAFYSGLG 72
Db 20 YRIMLETSLFVATLATLMLSPQDFLLIRNARYQRSAAWMTSLGVILGVATHWAYCV 79

Qy 73 FGLATLITQCEIEISLRIVGGAYLLWFAWCSMRQSTPQMSLTQOPIIS-----APWVVF 127
Db 80 AGLAVLITTTPLFNFALKYTGAVYLLWGIQIALSRGG---GILDVAVGVQVRGVHSAF 136

Qy 128 FRRLITOLSNPOTVLPFFISFVTLNAETPTWRLMAWAGIVLASIIRVVFSLQAFSL 186
Db 137 L-QGYLCNLLNPKATLFFLAVFTQVLSLDS-SFAEKLWYAGIIVGLAALWPLLVLIQS 194

Qy 187 PAVRRAYGRMORVASRVIGAI 208
Db 195 AVRRGLARAGGVVDKLLGGLL 216

RESULT 8
US-09-328-352-4775
; Sequence 4775, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4775
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4775

Query Match 19.4%; Score 220.5; DB 4; Length 210;
Best Local Similarity 26.7%; Pred. No. 1.9e-16;
Matches 54; Conservative 39; Mismatches 106; Indels 3; Gaps 1;

Qy 16 PLHAVYLTGVLFTVITFFNCGANLFFVVTSLASGRAGVLTGLGVALGDAFYSGLGFL 75
Db 10 PLFSIAMLMLGAI---SPGPSFIYVAQNSISKSRKHGLFTALGTGTGAALFGFLAVMGL 66

Qy 76 ATLITQCEIEISLRIVGGAYLLWFAWCSMRQSTPQMSLTQOPIISAPWVFFRGLITD 135
Db 67 QAVLAVPSAYLLIKGGGLYLLWLFKIKHAKPIAMENDAKSKMTYKQAVRYGLITQ 126

Qy 136 LSNPOTVLPFFISFVTLNAETPTWRLMAWAGIVLASIIRVVFSLQAFSLPAVRAYGR 195
Db 127 LSNPKIAVLVSVFVQVQIDVNAKTPGVAFVILALTLEIVSFYMSFLILSGSFVTRYV- 186

Qy 196 MORVASRVIGAIIGVFALRLIY 217
Db 187 AKTGVDVAGSIVSVLGLKLI 208

RESULT 9
US-09-328-352-8249
; Sequence 8249, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8249
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
```

US-09-328-352-8249

```

Query Match      19.4%; Score 220.5; DB 4; Length 235;
Best Local Similarity 26.0%; Pred. No. 2.2e-16;
Matches 56; Conservative 37; Mismatches 79; Indels 43; Gaps 6;

7 LFMDBITMDPLHAYLVTVGLVFITF-FNPGANLFFVVVQTSLSGRRRAGVLTGLGVALGDA 65
  19 IFFKDLSMLDLSQI-LAFGLICLAWLTTPGNMYILISRSISQGKIAGFISLGGVAVGVFV 77
  66 FVSGLGLRLATLTQCEETFSIRIVGGAYLLWLPFWCMMRQSTPQMSLTLLQQPISAPWY 125
  78 FYMLCASEGITALLVAVPYAYDITRIAGAYMLLWLAALKALRPNAAPIFNVKDLAVDSPLK 137
  126 VFRRGLTLDLSNPQTVLFTSIF-----SVTLNA----- 155
  138 LFL-MGFLTNLNPKIAIMVLSLLPQFIHQQSILAQSIQLGTGIQIFVSVSNALIVFS 196

156 -----EPTTWARLMAWA-GIVLASIIRVFL 180
  137 AGSIALFLQKKPLWASIQRWVMTGTVLAGLAVRILL 231

```

```

RESULT 10
US-09-252-991A-25992
; Sequence 25992, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25992
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25992

```

Query Match	18.2%	Score 207;	DB 4;	Length 260;
Best Local Similarity	27.3%;	Pred. No. 7.8e-15;		
Matches	57; Conservative	44;	Mismatches 94;	Indels 14; Gaps 4;

2Y	12	ITMDPLHAVLYTGLVFITFPFGANLFVVVQTSLASRRRAGVLTGVLGADPAYSIGL	71
bB	46	VAMQELSVLTAAVFAIALVSPGPVALVVRTSLHQHRRRASLAGLACILHTTLV	105
2Y	72	LFGIATLIQTCEIFSLIRIVGGAYLLWPAWCMSR---RSTPQMSTLQQQPTIS----	APW 124
bB	106	LTGVSLLSLRTPVFLFATLQALGALYLAWLGVGVALRAWLRRGDQPRLDGALPPSPLCPW	165
2Y	125	VYFFERGLINDLNPGQTVLPFISSIPVTNLNAETPTWARLMAGVILASIIWRVFLSQAF	184
bB	166	L-----RGVATNLFNPKALVLTLLALLGSLLPAQWSLGKLVAALLFGMGACMFWGLLSLT	221
2Y	185	SLPAVRRAYGRMQVRSRVGAIGVFAL	213
bB	222	TREPALQ----ARLLRAVEPWLDAACGVVFLL	247

RESULT 11
 US 09-483-039A-8849
 Sequence 8849, Application US/09489039A
 Patent No. 8610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

```

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8849
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8849

```

Query March	16.8*	Score 190.5	DB 4	Length 231
Best Local Similarity	27.0*	Pred. No. 4.5e-13		
Matches 60	Conservative 45	Mismatches 92	Indels 25	Gaps 7
Qy	11	ETMDPLHAYV-----LTGGLVFITTFNPGANLFVVVQTSLASGRAGVLTGLGVALGD	64	
Db	8	EATMHTLSTLFPVFPALASHFV-ALLSGPDFLLIGYAVRYIRGSGLCGLGIAAGN	66	
Qy	65	AFTSGGLGFLGTLTITOCBIFSLIRIVGGYALWPAWCSMR-RQSTPQMSTLQOIPISAP	123	
Db	67	ALYIVLAIVGWG-LLRQAPLFLFLLIELLGAGYLWIGSLLIRSPATLAMESVRAARDPGF	125	
Qy	124	WYVFFRRGLTLDLSNPOTVLFFFISIF-----SVTLNAETPTWARLMAWAGIVLASII--	175	
Db	126	GRQLLLGLGSLNPNKALFYALMTSLTGLGPATVLLQQIV-----SGLWVSVVFP	177	
Qy	176	WRVFLSQAFSLPAVRRAYGMQRVASRVIGALIGVFALRIIY	217	
Db	178	WDLLLSVSAIPQTQIRRLGAIWVRVERAAGAILMLFGLGIHW	219	

RESULT 12
US-09-543-681A-4854
; Sequence 4854, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4854
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4854

[illegible]

Db 122 NPKTAIFVIAFLPQFINTSLDPPVWSQF-----IILGLIVNLIFVS 162

RESULT 15
US-09-710-279-708
; Sequence 708, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 708
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-708
Query Match 15.8% Score 179; DB 4; Length 210;
Best Local Similarity 23.4%; Pred. No. 7,5e-12;
Matches 49; Conservative 51; Mismatches 99; Indels 10; Gaps 6;
QY 14 MDPLHNVLTGVLVITTFNPGANLFFVVQTSLSAGRRAGVLTGLGVALGDAPFYSGLGLF 73
DB 1 MDGL-ITFIITLILIV--PGDFIIVMKNITNSKMGFMFAFGITTHLYSLAIF 57
QY 74 GLATLITQCEIFSLIBIVGAYLWFAWCS-MRQSTPQMS--TLQOPISAPWYVFFRR 130
DB 58 GIYIITLSLHFVLTILKLGACLIYLGIKSILSAHSSVDFSKQALADVRNVSYITSFRQ 117
QY 131 GLITDLSNPQTVLHFISFVTL--NAETPTWALMAWAGIVLASIIRVFLSQAFSLP 187
DB 118 GLFSLNPLKALLFYVIFPQFLSNGNIHKSEVALFAPS-VVVVICLWFLFCVFIQYI 176
QY 188 AVRRAYGRMQRVASRVIGALIGVFALRI 216
DB 177 KLLFSRPRFAIFDYVINGVILIGLSINLL 205

Search completed: January 25, 2005, 16:45:50
Job time : 41 secs

RESULT 13
US-09-328-352-4784
; Sequence 4784, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4784
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4784
Query Match 16.4% Score 186; DB 4; Length 206;
Best Local Similarity 23.5%; Pred. No. 1.2e-12;
Matches 47; Conservative 51; Mismatches 98; Indels 4; Gaps 2;
QY 19 AVYLTGVLG-F-VITFENPGANLFFVVQTSLSAGRRAGVLTGLGVALGDAPFYSGLGLFGLAT 77
DB 6 AEPIAVILITILAVVSPGADFAIVTKNSYLGKIGVFTSLGSLGVLHVTVTLVAVTF 65
QY 78 LITQCEIFSLIRIVGAYLWFAWCS-MRQSTPQMS--TAIGTFOAIKYGFFTNAL 122
DB 66 VMTYTPQILNIVKYICALYLIYIGYKTFQKPVLDAAAL--TAIGTFOAIKYGFFTNAL 122
QY 138 NPQTVLFFISFVTINAEPTWALMAWAGIVLASIIRVFLSQAFSLPARRAYGRMQ 197
DB 123 NPKTTLFVISTVQTSVITPKTVLLAYGFFMSFAHFVWFLVAMLFSSMLLRQMLAKQ 182
QY 198 RVASRVIGALIGVFALRIY 217
DB 183 VQINKVIGSLLCVLGVLLF 202

RESULT 14
US-09-328-352-5111
; Sequence 5111, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5111
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5111
Query Match 16.0% Score 182; DB 4; Length 208;
Best Local Similarity 27.7%; Pred. No. 3.4e-12;
Matches 46; Conservative 43; Mismatches 63; Indels 14; Gaps 7;
QY 20 VYLTGVLVITF-FNPG-NLFFVVQTSLSAGRRAGVLTGLGVALGDAPFYSGLGLFGLAT 77
DB 7 LFTFLITTIIFAIIFPAPMLTAAQT-LSGRKSLGMAAFGI FVGGCFHIAASLGLTT 65
QY 78 LITQCEIFSLIRIVGAYLWFAWCS-MRQSTPQMS--TLQONVE-NGQLSLRQILVEVL 121
DB 66 IQPIPKLYDILKLGALYLVWGLKLRSTSSP--TLQONVE-NGQLSLRQILVEVL 121
QY 138 NPQTVLFFISFVTINAEPTWALMAWAGIVLASIIRVFLSQAFSLPARRAYGRMQ 197

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 16:37:59 ; Search time 145 Seconds
(without alignments)
555.638 Million cell updates/sec

Title: US-09-459-573-10
Perfect score: 1135
Sequence: 1 MQLVHLFMDIEITMDPLHAV.....IGAILGVFAIRLIYGVTVQR 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	19.1	226	9	US-09-738-626-3665
2	179	15.8	207	9	US-09-738-626-6418
3	175	15.4	217	14	US-10-156-761-10918
4	168	14.8	205	14	US-10-156-761-11297
5	166	14.6	223	9	US-09-738-626-6070
6	166	14.6	223	17	US-09-746-660A-14
7	166	14.6	223	17	US-10-494-672-256
8	162	14.3	212	15	US-10-374-903A-5
9	145.5	12.8	206	15	US-10-282-122A-78024
10	143	12.5	209	15	US-10-282-122A-6884
11	141.5	12.5	206	15	US-10-282-122A-75782
12	140.5	12.4	224	14	US-10-156-761-7796
13	138.5	12.2	205	15	US-10-282-122A-76964

ALIGNMENTS

RESULT 1
US-09-738-626-3665
; Sequence 3665, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3665
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3665

Query Match 19.1%; Score 217; DB 9; Length 226;
Best Local Similarity 28.6%; Pred. No. 2e-14;
Matches 63; Conservative 48; Mismatches 81; Indels 28; Gaps 7;

Sequence 72863, A
Sequence 47826, A
Sequence 94, Appl
Sequence 124, App
Sequence 56211, A
Sequence 51102, A
Sequence 2, Appl
Sequence 2, Appl
Sequence 60157, A
Sequence 67883, A
Sequence 69338, A
Sequence 8659, Ap
Sequence 14994, A
Sequence 5, Appl
Sequence 44873, A
Sequence 2, Appl
Sequence 56075, A
Sequence 43089, A
Sequence 69966, A
Sequence 59719, A
Sequence 64286, A
Sequence 73496, A
Sequence 76048, A
Sequence 52, Appl
Sequence 25, Appl
Sequence 6955, Ap
Sequence 8, Appl
Sequence 8, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 8, Appl
Sequence 78364, A

Qy	19	AVYLTVGLVFITVFNFPGANLFFVVVQTSLASGRRAGVLTGLGVALGDAPYSGLGLFGIATL	78
Db	8	ALFLF---VMIAAIASGPGDLPQIIRLS-AKRRDGVLTAVGIMVGSNIWIIASLGLSAL	63
Qy	79	ITQCEEIFSLIRIVGAYLLNFAWCMR-----RSTPMOSTLQOPI-----SAPW	124
Db	64	ISTYPAILNLLGVGGVLTWVGIGAVRSMWTKRSTQQAADSQAVENTLVTATAASGV	123
Qy	125	YVFFRRGLITDLSNPQTVLFFPISFVTLNAETPTWARLMAWAGIVLASIIWRFVLSQAF	184
Db	124	WPAIRSGIATNLSNKPVLVFCSPVPAQVFRDPMGIHGSIFIGVFLTUTGLWFV----	179
Qy	185	SLPAPVRAYGRMQRVASRVIGAIIVFAIRL-----IYEGV	220
Db	180	AVLVRKLAAGLRNGA--IIDLLGTVPFIGLGMFWIEGV	217

RESULT 2

US-09-738-626-6418
; Sequence 6418, Application US/09738626
; Publication No. US20020197605A1

/ GENERAL INFORMATION:
 / APPLICANT: NAWAGAWA, SATOSHI
 / APPLICANT: MIZOGUCHI, HIROSHI
 / APPLICANT: ANDO, SEIKO
 / APPLICANT: HAYASHI, MIKURO
 / APPLICANT: OCHIAI, KENJI
 / APPLICANT: YOKOI, HARUHIKO
 / APPLICANT: TATEISHI, NAOKO
 / APPLICANT: SENOH, AKIHIRO
 / APPLICANT: IKEDA, MASATO
 / APPLICANT: OZAKI, AKIO
 /

```

, , TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
, , FILE REFERENCE: 249-125
, , CURRENT APPLICATION NUMBER: US/09/738,626
, , CURRENT FILING DATE: 2000-12-18
, , PRIOR APPLICATION NUMBER: JP 99/377484
, , PRIOR FILING DATE: 1999-12-16
, , PRIOR APPLICATION NUMBER: JP 00/159162
, , PRIOR FILING DATE: 2000-04-07
, , PRIOR APPLICATION NUMBER: JP 00/280988
, , PRIOR FILING DATE: 2000-08-03
, , NUMBER OF SEQ ID NOS: 7059
, , SOFTWARE: PatentIn ver. 3.0

```

```

; SEQ ID NO 6418
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6418

```

Query Match	15.8%;	Score 179;	DB 9;	Length 207;
Best Local Similarity	31.6%;	Pred. No. 1.8e-10;		
Matches 65; Conservative	32;	Mismatches 87;	Indels 22;	Gaps 9.

[illegible]

RESULT 3

```

US-10-156-761-10918
; Sequence 10918, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10918
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10918

```

	Query Match.	15.4%;	Score 175;	DB 14;	Length 217;
	Best Local Similarity	27.9%;	Pred. No. 5.2e-10;		
	Matches	60;	Conservative	34;	Mismatches 97; Indels 24; Gaps 8;
Qy	21 YLTVG ^L FVITFFPFGANLFFVVQTSLASGRAGVLTLGLVALGDAPFYSGILFLGLATLIT	80			
Dd	10 YL-AGLVLI ^{VLL} -PGPNLSYLVLSVAARKGV ^R GVTAAAGVWC ^G TIVMLTSAAGVASL ^{UQ}	67			
Qy	81 QCSEIFSLIRIVGAYLLWFAWCSMR-----RQSTPQMSTLOQPIS-----APWYVF ^{FR}	129			
Dd	68 ANALLF ^{GI} VKYAGAYLTWLAFGLRAAEMWMTRRDRADAARPAVPVAGERP----FR	123			
Qy	130 RGLITDLSNPOTVLFFTSIP--SVTLNAEPTWARLMAWAGIVLASIIWRVFLSQASLP	187			
Dd	124 RAFVSLFPKALLFVAFVQVDGYYPALUSFVVLGAFAQLASPLYLTAL--I ^{ESGT}	181			
Qy	188 AVRRAYGRMQRV---ASRVIGAI ^{GV} FALRLIYEG	219			
Dd	182 KLA ^A AAPFRKRISAGATTAAAGALFLCGFAVKLTLAG	216			

RESULT 4

```

RESUL* 4
US-10-156-761-11297
; Sequence 11297, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11297
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11297

```

Db	185	ERVKAMLRAGPWFLLAGVFLVGVVTLLEYGLT	219
RESULT 6			
US-09-746-660A-14			
; Sequence 14, Application US/09746660A			
; Publication No. US2003004980A1			
; GENERAL INFORMATION:			
; APPLICANT: Pompejus, Markus			
; APPLICANT: Kroger, Burkhard			
; APPLICANT: Schroder, Hartwig			
; APPLICANT: Zelder, Oskar			
; APPLICANT: Haberhauer, Gregor			
; APPLICANT: Kim, Jun-Won			
; APPLICANT: Lee, Heung-Schick			
; APPLICANT: Hwang, Byung-Joon			
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING			
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS			
; FILE REFERENCE: BGI-121CP2			
; CURRENT APPLICATION NUMBER: US/09/746,660A			
; CURRENT FILING DATE: 2000-12-22			
; PRIOR APPLICATION NUMBER: 09/606740			
; PRIOR FILING DATE: 2000-06-23			
; PRIOR APPLICATION NUMBER: 09/603124			
; PRIOR FILING DATE: 2000-06-23			
; PRIOR APPLICATION NUMBER: 60/141031			
; PRIOR FILING DATE: 1999-06-25			
; PRIOR APPLICATION NUMBER: 60/142101			
; PRIOR FILING DATE: 1999-07-02			
; PRIOR APPLICATION NUMBER: 60/148613			
; PRIOR FILING DATE: 1999-08-12			
; PRIOR APPLICATION NUMBER: 60/187970			
; PRIOR FILING DATE: 2000-03-09			
; PRIOR APPLICATION NUMBER: DE 19931420.9			
; PRIOR FILING DATE: 1999-07-08			
; NUMBER OF SEQ ID NOS: 125			
; SOFTWARE: PatentIn Vers. 2.0			
; SEQ ID NO 14			
; LENGTH: 223			
; TYPE: PRT			
; ORGANISM: Corynebacterium glutamicum			
US-09-746-660A-14			
Query Match			
Best Local Similarity			
Matches			
Query Match			
Best Local Similarity			
Matches			
Qy	26	LFVITFFNPGANLFVVVQTSLSAGRRAGVITGL-GVALGDFAFYSGLGFLGLATLITQCEE	84
Db	12	LNLVGLSLSPGPDPTFFLLR--LATRSRAHAIAAGVAGIVTGLTWVTLTVVGAALLTTPYS	69
Qy	85	IFSLIRIVGGAYLLWFAMCSMRQSTQMSTLQOPIISA-----PMYV-----PFPRG	131
Db	70	ILGIIQLVGGTYSFGYKLLRSARELIDARQFRFNADARPIDPAVEALGTRTQVYRQG	129
Qy	132	LITDLSNPQTVLPFFISFVTLNAETPTWARLMAWAGIVLASIIRVFLSQA-----FSL	186
Db	130	LATLNSNPKVMYFAAILAPLMPAHP---SPVLAFS--IIIVAILQTVFTFSAVCLIVST	184
Qy	187	PAVRAYGRMQRVASRVIGAILGVFALRLIYEGVT	221
Db	185	ERVKAMLRAGPWFLLAGVFLVGVVTLLEYGLT	219
RESULT 7			
US-10-494-672-296			
; Sequence 296, Application US/10494672			
; Publication No. US2005000349A1			
; GENERAL INFORMATION:			
; APPLICANT: Zelder, Oskar			
; APPLICANT: Pompejus, Markus			
; APPLICANT: Schroder, Hartwig			
; APPLICANT: Kroger, Burkhard			
US-10-494-672-296			
Query Match			
Best Local Similarity			
Matches			
Qy	26	LFVITFFNPGANLFVVVQTSLSAGRRAGVITGL-GVALGDFAFYSGLGFLGLATLITQCEE	84
Db	12	LNLVGLSLSPGPDPTFFLLR--LATRSRAHAIAAGVAGIVTGLTWVTLTVVGAALLTTPYS	69
Qy	85	IFSLIRIVGGAYLLWFAMCSMRQSTQMSTLQOPIISA-----PMYV-----PFPRG	131
Db	70	ILGIIQLVGGTYSFGYKLLRSARELIDARQFRFNADARPIDPAVEALGTRTQVYRQG	129
Qy	132	LITDLSNPQTVLPFFISFVTLNAETPTWARLMAWAGIVLASIIRVFLSQA-----FSL	186
Db	130	LATLNSNPKVMYFAAILAPLMPAHP---SPVLAFS--IIIVAILQTVFTFSAVCLIVST	184
Qy	187	PAVRAYGRMQRVASRVIGAILGVFALRLIYEGVT	221

```
; APPLICANT: Klopprogge, Corinna
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: Genes coding for novel proteins
; FILE REFERENCE: BGI-169US
; CURRENT APPLICATION NUMBER: US/10/494,672
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: PCT/EP02/12134
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: DE 10154177
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 434
; SEQ ID NO 296
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-494-672-296

Query Match 14.6%; Score 166; DB 17; Length 223;
Best Local Similarity 26.0%; Pred. No. 4.7e-09;
Matches 56; Conservative 50; Mismatches 83; Indels 26; Gaps 7;

Qy 26 LFVITFNPNGANLFVVVQTSLSGRRAGVLTGL-GVALGDAFYSGLGFLGLATLIQCEE 84
Db 12 LNLVGSLSPGDFFELLR--LATRSRAHAAGVAGIVGLTWVTLTVVGAALLITYPS 69

Qy 85 IFSLRIVGAYLLWFACSMRRQSTPQMSLQOPISA-----PWVY-----FFRRG 131
Db 70 ILGIQLVGGTYSFGYKLLRSASRELIDARQFRENADARPDPDAVEALGTRTQVYRQG 129

Qy 132 LITDLNPNQTVLFFISFVTLNAETPTWARLMAMAGIVLASIIRVFLSQA-----PSL 186
Db 130 LATNLNPKVMYFAAILAPLMPAHP---SPVLAFS---IIVALLVQTFVTSFSAVCLIVST 184

Qy 187 PAVRRAYGRMQRVASRVIGAIIGVFALRIYEGVT 221
Db 185 ERVRKAMLRAGPWFDDLGVGVFLVGVGVTLLYEGLT 219

RESULT 8
US-10-374-903A-6
; Sequence 6, Application US/10374903A
; Publication No. US20040038250A1
; GENERAL INFORMATION:
; APPLICANT: University of Oviedo
; APPLICANT: Actur Pharma, S.A.
; TITLE OF INVENTION: The gene cluster for thienamycin biosynthesis,
; FILE REFERENCE: Thienamycin-UC-AP
; CURRENT APPLICATION NUMBER: US/10/374,903A
; CURRENT FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 6
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptomyces cattleya
US-10-374-903A-6

Query Match 14.3%; Score 162; DB 15; Length 212;
Best Local Similarity 25.3%; Pred. No. 1.2e-08;
Matches 58; Conservative 36; Mismatches 93; Indels 42; Gaps 8;

Qy 14 MDPLHAVYLT-YGLFVITFFNPNGANLFVVVQTSLSGRRAGVLTGLGVALGDAFYSGLGL 72
Db 1 MEPMITLALAFAGACVLIAAPGPSTMLIIIRQSLHS--BRAGFLTVLGNETGVLTWGVVAA 59

Qy 73 FGLATLITQCEBIFSLIRIVGAYLLWFACSMR-----RQSTPQMSLQOPIAPWY 125
Db 60 LGLTALLAASRTAYDVMRIGGAVLVGVQTLRAARGEARPSADDEAAVVRSG-WK 118

Qy 126 VFPRGLTDLNPNQTVLFFISFVTLNAETPTWARLMAMAGI-----VLASIIWRV 178
Db 119 I-YRSGLLNLNPNKAAVFAVMSFLPQFVPAGAPKLPVITALLAFAQALFEVGYGYGVVWFV 177
```

```
Qy 179 FLSQAFSLPAVRRAYGRMQRVASR-----VIGAIIGVFALRLIYE 218
Db 178 -----GRMKRVISRAGVRRRLRLEQVSGGVVLIGIRWAVE 211
```

RESULT 9

```
US-10-282-122A-78024
; Sequence 78024, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlssen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78024
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Versinia pestis
US-10-282-122A-78024
```

```
Query Match 12.8%; Score 145.5; DB 15; Length 206;
Best Local Similarity 23.8%; Pred. No. 6.2e-07;
Matches 49; Conservative 46; Mismatches 96; Indels 15; Gaps 5;
```

```
Qy 12 ITMDPLHAVYLT-VGLFVITFFNPNGANLFVVVQTSLSGRRAGVLTGLGVALGDAFYSGLG 71
Db 1 MTLDDWMLTYLLTT--LILSLSPGSAINTMTSTAISHGTRGVVVASIGGLQLGLAVHIVLV 57

Qy 72 LFGLATLITQCEBIFSLIRIVGAYLLWFACSMRRQSTPQMSLQOPIAPWYVFRG 131
Db 58 GVGLGALVQSLLAFILKWLGNAYLIWLGIQWRAGSLDLHALAN--SMPRKLFKKA 115

Qy 132 LITDLNPNQTVLFFISFVTLNAETPTWARLMAMAGIVLASIIRVFLSQAFLPAVR 191
Db 116 VFVNLNPKSVFLAALFPQVLPQOPQVAQVILGS---TSVIVDIIWIGVATLATRI 172

Qy 192 A----YGRMQRVASRVIGAIIGVFAL 213
```

Db 173 ARWIKSPQMKLLNRIFG---GLFML 195

RESULT 10
US-10-282-122A-66814
; Sequence 66814, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2003-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66814
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66814

Query Match 12.6%; Score 143; DB 15; Length 209;
Best Local Similarity 25.6%; Pred. No. 1.2e-06;
Matches 53; Conservative 39; Mismatches 89; Indels 26; Gaps 9;
QY 26 LFVITFF-----NPGANLFVVVQTSLSAGRRAGVLTGLGVALGDAFYSGGLGSG 74
Db 1 MLVSTWFAFFLACWAISLSPGAGATASCGLOQYGFARGYNALGQIGLALQIAIVAG 60
QY 75 LATLITQCEIFSLIRIVGGAYLLWFA---WCSMRQSTTQ-MST-LOQPISAPWVYFFR 129
Db 61 VGALLATSAFAFLSKWGFAYLVLAVRW-----QAPPQALSTGGERPUGRP-LTLVL 114
QY 130 RGLITLDSNPQTVLFFSIFSVTLNAETPTWARIMAWAG--IVLASIIRVFLSQPSLP 187
Db 115 RGFVNASNKAVIFMLVLPQIDPQPLLAQYLLMGTMIVDVLVMAGYTGLAARVL 174
QY 188 AVREAYGRMQRVASRVIGAI-IGVFPAL 213
Db 175 RVLRSPROQKLVNRTFASLFVGAAGL 200

RESULT 11

US-10-282-122A-75782
; Sequence 75782, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75782
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Salmonella typhi

US-10-282-122A-75782

Query Match 12.5%; Score 141.5; DB 15; Length 206;
Best Local Similarity 24.2%; Pred. No. 1.6e-06;
Matches 52; Conservative 46; Mismatches 84; Indels 33; Gaps 8;
QY 12 ITWDPILHAVVLTGVLVITFFNPGANLFVVVQTSLSAGRR-----AGVLTGLGVALGDA 65
Db 1 MTPFWWFAVLLTSTLLSL---SPGSGAINTMTTTSINHGYRGAASIAAGLOTGLGI----- 52
QY 66 FYSGLGLFGLATLITQCEIEIFSLIRIVGGAYLLWFAWCSMRQSTTQPMSTLQQPISAPWY 125
Db 53 -HIVLVGVGLGTLFSSRLIAFEILKWAGAAVLIWLGIQOWRAAGAIIDLHTUAQTQSRG-- 109
QY 126 VFFRGLITLDSNPQTVLFFSIFSVTLNAETPTWAR--LMWAGIVLASIIRVFP--LS 181
Db 110 RLFKRAIFVNLINPKSIVFLAALFPQFIMPQPOLAQYLLGLVTTIVVDMIVMTGYATLA 169
QY 182 QAFS-----LPVRRAYGRMQRVASRVIGAI 208
Db 170 QRIAAWIKGPKQMKALNKAFGSL---FMLVGALL 200

RESULT 12

```
US-10-156-761-7796
; Sequence 7796, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7796
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7796

Query Match      12.4%; Score 140.5; DB 14; Length 224;
Best Local Similarity 22.4%; Pred. No. 2.3e-06;
Matches 46; Conservative 38; Mismatches 78; Indels 43; Gaps 6;

QY 24 VGLFVITFFNPGANLVVVQTSI---ASGRAGVLTLGVALGDAPYSGLGLFGLATLIT 80
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
9 LGVVVAVYVPGDFLWVRSATEHPAKGRAA-----ALGAQSGCLCVHMLAAAVGLSLIAA 64
QY 81 QCEIEFSLIRIVGGAYLLWF---AWCSMRQ-----STPQMSLTLOQPI 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 RSPAVDAIRLLGAAVVLGVAVLAARRAARERAAAGREAVGGVEDGDPRTPEEAPA 124
QY 121 SAPWYVFRGLITLDSNPQTVLFFISFVTLNAETPTWARLM-----AWAG 168
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 HGRWRSQGTQGLTFLVNLNPKAALFFLSILPQFVHGGGTSRQIFFLGLTLDIVIGVAYWFA 184
QY 169 IVLASIIWRVLSQAFSLPAVRAY 193
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 LVAAARLARAFAR-----PKVRHG 205

RESULT 13
US-10-282-122A-76964
; Sequence 76964, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

US-10-282-122A-72863
; Sequence 72863, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

US-10-282-122A-76964
; Sequence 76964, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
```


THIS PAGE BLANK (uspto)

Db 187 CTATCCAGCTGATGGCCATTGCGCGGTGCTGATCATGGCGTGCATGCCGCGCCA 246
Qy 37 AnLeuPheValValGlnThrSerLeuAlaSerGlyArgAlaGlyValLeuThr 56
Db 247 AGCTTTATTTTTCGCGCGCAATGCGTGCCTGCGTGTGCACGGTATGTCGACC 306
Qy 57 GlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAla 76
Db 307 GCCTTCGTACCGCGCGGTGGCGCAATTTTCCTATGCGGATGTCGGCGCTGCAG 366
Qy 77 ThrLeuThrGlnCysGluGluThrPheSerLeuLeuArgLeuValGlyAlaTyr 96
Db 367 AAGTGCTCACGCGGTGCGGAGCTGTTTATGTTTGAAGTGGCGGCGGCTCTAT 426
Qy 97 LeuLeuThrPheAlaTyrCysSerMetArgArgGlnSerThrPro--GlnMetSerThr 115
Db 427 CTGCTGTGGTGGGTATAAATTTTCGCGGTGCGCGAGCGATGTCGCTTTCGCC 486
Qy 116 LeuGlnGlnProIleSerAlaProTyrValPhePheArgArgGlyLeuLeuThrAsp 135
Db 487 AGCGGATGGCGCGCACCGCTCTTGTCTGAAGACCTTCGCGACGGCTGTACTCAG 546
Qy 136 LeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAla 155
Db 547 CTGCGATCCCAAACTGCGTGGTTCGCTCAATTTTACCGCCCTGCTCGCGCG 606
Qy 156 GluThrProThrTyrAlaArgLeuMetAlaTyrAlaGlyIleVal----- 170
Db 607 CAGTCCCGCC-----GCTTCTATTACATGTCGCGCGTGCATGAGCTTT 651
Qy 171 LeuAlaSerIleThrArgValPheLeuSerGlnAlaPheSerLeuProAlaValArg 190
Db 652 CTATCGAGTCAGCTGGTATTCCTGGTGGCGTGGTCTGTCGCGACCGCGCG 711
Qy 191 ArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyVal 210
Db 712 CGGCTCTACTCGGCTGAAGCGCGGATCGATCGCACGCGCGTGCCTGGCGGG 771
Qy 211 PheAlaLeuArgLeuIleTyrGluGlyValThrGln 222
Db 772 CTGGGCTGGGCTTATCGCCACCTCCCTCACCAGC 807
RESULT 4
US-09-328-352-2569
; Sequence 2569, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: SAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2569
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2569
Alignment Scores:
Pred. No.: 1,29e-20 Length: 645
Score: 237.50 Matches: 59
Percent Similarity: 50.50% Conservative: 42
Best Local Similarity: 29.50% Mismatches: 96
Query Match: 20.93% Indels: 3
DB: 4 Gaps: 2
US-09-459-573-10 (1-223) x US-09-328-352-2569 (1-645)
Qy 21 TyrLeuThrValGlyLeuPhe---ValIleThrPhePheAsnProGlyAlaAsnLeuPhe 39
Db 31 TTTTAAACGCTAGCTCTTATTCACTTTATGCGCGTGTATTTACCGGACGACGATTTTGTG 90

Qy 40 ValValValGlnThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGlyLeuGly 59
Db 91 ATTACGGTACGACAAAGTATGCTATGCTATGTTGTTGCTGCTGCTGCTGCTGCTGCT 150
Qy 60 ValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIle 79
Db 151 ATTGTGTGCGCAATTTTCAGTCCATGTTTATACATGTTGTTGTTGTTGTTGTTGTTGTT 210
Qy 80 ThrGlnCysGluGluThrPheSerLeuLeuArgLeuValGlyAlaTyrLeuLeuThr 99
Db 211 CAGCAAAAGTAAATGCTTATGTCACATGATCAGACAGCGGGGGGGGCTTACTAGTAT 270
Qy 100 PheAlaTyrCysSerMetArgArgGlnSerThrProGlnMetSerThrLeuGlnGlnPro 119
Db 271 TTAGGATGGCAGTCTTACGTACCGACCGAATACCAATATTGAAATTAATGCCCAATTA 330
Qy 120 IleSerAlaProTyrTyrValPhe-----PheArgArgGlyLeuIleThrAspLeuSer 137
Db 331 GACGTGACACCGCGAGTTTATTTAAAGCGTTTACAATGGGTTTTCTCACTAATGCGTTA 390
Qy 138 AsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAlaGluThr 157
Db 391 AACCCCAAGCCACCATCTTTTCTGCGCAATTTTACGACGATTGTAAGTACGACCACA 450
Qy 158 ProThrTyrAlaArgLeuMetAlaTyrAlaGlyIleValLeuAlaSerIleIleThrArg 177
Db 451 CCAATGAAAGTTTCAGGTTTATATGGGGTTGATGTTGATGTTGTTGTTGTTGTTGTTGTT 510
Qy 178 ValPheLeuSerGlnAlaPheSerLeuProAlaValArgAlaTyrGlyArgMetGln 197
Db 511 ATGGTGGTGGTGTACTGTTTGCACAGCCTATCGTACGTAAGAAAGATTTTGGAGTTGGG 570
Qy 198 ArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyr 217
Db 571 GTTTATTTTGAGAGGTTGATGGGAGTGTATTATTAATGGAATTCATTCAGATTGATTGG 630
RESULT 5
US-09-252-991A-2095
; Sequence 2095, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2095
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2095
Alignment Scores:
Pred. No.: 3,76e-19 Length: 651
Score: 226.00 Matches: 58
Percent Similarity: 51.27% Conservative: 43
Best Local Similarity: 29.44% Mismatches: 90
Query Match: 19.91% Indels: 6
DB: 4 Gaps: 3
US-09-459-573-10 (1-223) x US-09-252-991A-2095 (1-651)
Qy 21 TyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheVal 40
Db 55 TTCTGACCATC-----ACTGTGCTGCGTGTATCAGCCCCGGCGGATTTGCCCATG 108

```

Qy 41 ValValGlnThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGlyLeuGlyVal 60
Db 109 GTCTCGGCAACACGCTGTATTCGCGCGCGCGCTGTCTACCGCGCTGGGCATC 168
Qy 61 AlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuThr 80
Db 169 GGC CGCGGGGTAACGGTACATGTCGGCTACAGCATCTCGCGCTCGCGCTGGTGGCGC 228
Qy 81 GlnCysGluGluLeuPheSerLeuLeuArgIleValGlyValGlyAlaTyrLeuThrPhe 100
Db 229 GAGTCGCTGGCGCTGTTCACCGCGCTGAGAGCTGCGCGCGCGCTACCTGCTGCTC 288
Qy 101 AlaTrpCysSerMet-----ArgArgGlnSerThrProGlnMetSerThrLeuGlnGln 118
Db 289 GGCCTGGCGCATGCTGCTGGCGGAGAGAGACTCGGTGCGGAGGAGGCGCGCGCGCGC 348
Qy 119 ProfileSerAlaProTyrValPhePheArgArgGlyLeuLeuThrAspLeuSerAsn 138
Db 349 GGGGTTCGTGCC-----TGGGCGATGTCGCGAGCGGCTTCCTGACCAATGCGCTCAAT 402
Qy 139 ProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAlaGluThrPro 158
Db 403 CCGAAGACCTGCGCTGTCGGGTGTCAGCTGTCATGCGGTGATCGATCGCATACCGCG 462
Qy 159 ThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAlaSerIleIleTrpArgVal 178
Db 463 TTCGCGCGCAACTGCGGTACGCGGCGCTTCATCGCGCTCGCCACGCTGCTGCTGCGC 522
Qy 179 PheLeuSerGlnAlaPheSerLeuProAlaValArgAlaTyrGlyArgMetGlnArg 198
Db 523 CTGCTGCGCTGCTTCTCTGACCGCGGCGGTGCGCGCGCTCCTGCGCTTTCGCGCGG 582
Qy 199 ValAlaSerArgValIleGlyAlaIleIleGlyValPheAlaLeuArgLeu 215
Db 583 CGCATCGACCACTCTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 633

```

RESULT 6

US-09-557-884-1

; Sequence 1, Application US/09557884
; Patent No. 6506581

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/557,884

; FILING DATE: 25-Apr-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,102

; FILING DATE: JUN-5-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Michelle S. Marks

; REGISTRATION NUMBER: 41,971

; REFERENCE/DOCKET NUMBER: PB186P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 1:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

```

```

Alignment Scores:
Pred. No.: 1,43e-13 Length: 1830121
Score: 225.00 Matches: 60
Percent Similarity: 44.78% Conservative: 43
Best Local Similarity: 26.09% Mismatches: 87
Query Match: 19.82% Indels: 40
DB: 4 Gaps: 4

```

US-09-459-573-10 (1-223) x US-09-557-884-1 (1-1830121)

```

Qy 4 LeuValHisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr 23
Db 1385069 ATTGTGCATTTATTT-----
Qy 24 ValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGln 43
Db 1385084 --GCATTA-----ATGACGCCAGCGCTGATTTCTTTTATGTAGTCGA 1385125
Qy 44 ThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGly 63
Db 1385126 ATGCGCGCAAGTAACCTCTCGTCAATACAGATTTGTGGCATTTTATGAGCATAACGCTTGGC 1385185
Qy 64 AspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu 83
Db 1385186 ATCCGCTTTGGGGAATGCTTTCTATGTTGGATGCGGTGTTGTTGTTACCATTTCCA 1385245
Qy 84 GluIlePheSerLeuIleArgIleValGlyGlyValTyrLeuLeuTrpPheAlaTrpCys 103
Db 1385246 GCATTACATGCGGTATATTGTTGCTAGTGGTAGTTTACCTAGCATATCTCGGTTTTTTA 1385305
Qy 104 SerMetArgArgGlnSerThrPro-----Gln 112
Db 1385306 ATGGCTCGCAGTAAATAACGTTAAATTCGACACTCTGATCTGATTAATTAATCAA 1385365
Qy 113 MetSerThrLeuGlnGlnProIleSerAlaProTyrValPhePheArgArgGlyLeu 132
Db 1385366 CAAACCAACAATCAAAAAGAAAT-----TTGAAAGGCGTT 1385401
Qy 133 IleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThr 152
Db 1385402 TTAGTGAATTTATCCAAATGCGCAATTAATCTCGCTTTTGCAGTGATTTGGTAGAA 1385461
Qy 153 LeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAla 172
Db 1385462 TTAGTAAATATCACTGAATGCGCAATTAATCTCGCTTTTGCAGTGATTTGGTAGAA 1385521
Qy 173 SerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgAla 192
Db 1385522 ACATTTGTTATTTTATGATTTTTCATTTTTCAGTAAATATTCGCAAGCGTTTA 1385581
Qy 193 TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleleGlyValPheAla 212
Db 1385582 TACAGTCAATACAGCGCTTATATTGATAATATGCGAGGATTGTTATTTTATTTTGTG 1385641
Qy 213 LeuArgLeuIleTyrGluGlyValThrGln 222
Db 1385642 TGTGTGCTTTTATTAACGGCATCAACGAA 1385671

```

RESULT 7

US-09-643-990A-1

; Sequence 1, Application US/09643990A

; Patent No. 6528289

; GENERAL INFORMATION:

; APPLICANT: Robert D. Fleischmann

; Mark D. Adams

Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186PlC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
Alignment Scores:
Pred. No.: 1,43e-13 Length: 1830121
Score: 225.00 Matches: 60
Percent Similarity: 44.78% Conservative: 43
Best Local Similarity: 26.09% Mismatches: 87
Query Match: 19.82% Indels: 40
Gaps: 4
DB:
US-09-459-573-10 (1-223) x US-09-643-990A-1 (1-1830121)
Qy 4 LeuValHisLeuPheMetAspGluLeuThrMetAspProLeuHisAlaValTyrLeuThr 23
Db 1385069 ATTGGCAATTATT----- 1385083
Qy 24 ValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValValGln 43
Db 1385084 ---GGATTA-----ATGACGCCAGGCGCTGATTCTTTATGTAGTCGA 1385125
Qy 44 ThrSerLeuAlaSerGlyValArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGly 63
Db 1385126 ATGGCGCAAGTAACTCTCGTGTAAATACAGTTGTGGCATTTAGGCATAACGCTTGGC 1385185
Qy 64 AsplapherTyrSerGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu 83
Db 1385186 ATCCGCTTTTGGGAATGCTTTCAAGTGGGATTGGCGTGTGTCTGTTACCAATCCA 1385245
Qy 84 GlullePheSerLeuIleargIleValGlyValAlaTyrLeuThrPheAlaTrpCys 103
Db 1385246 GCATTACATCGCGTTATTATGTGTAGGTAGTTACCTAGCATATCTCGGTTTTTTA 1385305

Qy 104 SerMetArgArgGlnSerThrPro-----Gln 112
Db 1385306 ATCGCTCCACTAAATAACGCTAAATTTGAATCGCACTCTGATCTGAATTAATCAA 1385365
Qy 113 MetSerThrLeuGlnGlnProIleSerAlaProTyrValPhePheArgArgGlyLeu 132
Db 1385366 CAATCCACATCAAAAGAAAT-----TTGAAAGGGCTT 1385401
Qy 133 IleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThr 152
Db 1385402 TTAGTGAAATTTATCCAAATGCAAAAGTCTGGGTATTTTAGTAGCGTGATGCTTGTG 1385461
Qy 153 LeuAsnAlaGluThrProThrTpAlaArgLeuMetAlaTpAlaGlyIleValLeuAla 172
Db 1385462 TTAGTAATATCACTGAAATGCGCAATATCTGGCTTTTGCAGTGATTGGTAGAA 1385521
Qy 173 SerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgAla 192
Db 1385522 ACATTTGTTATTTTATGTGATTTCTTGATTTTTCACGTATATATGCAAGCGTTTA 1385581
Qy 193 TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAla 212
Db 1385582 TACAGTCAATACAGCGGTATATATGATATATGCGAGTATTTGTTATTTTGTG 1385641
Qy 213 LeuArgLeuIleTyrGluGlyValThrGln 222
Db 1385642 TGTGCTCTGTTTATAACGGCATCAACGAA 1385671
RESULT 8
US-10-329-960-1
; Sequence 1, Application US/10329960
; Patent No. 6742927
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra
; TITLE OF INVENTION: Thereof, and Uses Thereof
; Patent No. 6742927
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10150)..(10150)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (29298)..(29298)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36543)..(36543)
; OTHER INFORMATION: n equals a, t, g or c

```
FEATURE:
NAME/KEY: misc feature
LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (36836)..(36836)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
```

```
NAME/KEY: misc feature
LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
```

```
; Sequence 560, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 560
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-560

Alignment Scores:
Pred. No.: 6,9e-19 Length: 660
Score: 224.00 Matches: 67
Percent Similarity: 50.00% Conservative: 36
Best Local Similarity: 22.52% Mismatches: 88
Query Match: 19.74% Indels: 16
DB: 4 Gaps: 6

US-09-459-573-10 (1-223) x US-09-489-039A-560 (1-660)
QY 18 HisAlaValThrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAan 37
DB 49 TATTAACTATCTGGTCGGGGGGTGTATCATCTCGTT-----CTGGCCCTAAT 102
QY 38 LeuPheValValGlnThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGly 57
DB 103 ACCTTTTCTGCTGAAACCGGTATTCGCCGGGTGAAAGAGCTATCTGGCGCG 162
QY 58 LeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThr 77
DB 163 GCGGGCGTCTTTATTTGGGCGAGCGAGTCTGATGTTTCTGGCTTCGCGGGTGGCGAG 222
QY 78 LeuIleThrGlnCysGluGluIlePheSerLeuIleAlaGlyValGlyAlaThrLeu 97
DB 223 CTGATTAAACACCCAGTGTGTGTACGTCGCTATCTCGGGCAATTACCTG 282
QY 98 LeuTrpPheAla-----TrpCysSerMetArgArgGlnSerThrProGlnMetSer 114
DB 283 CTGTGGCTCGGGGCAAAATCTCTATCGGTGCTGACCCAGCGCGAGCCAGTCCGAC 342
QY 115 ThrLeuGlnProIleSerAlaProTyrTrpValPhePheArgGlyLeuThr 134
DB 343 GCGAGCGCGAGCGCGGCGAGCGG-----ATCTCAAGCTCCCTGACCTG 390
QY 135 AspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePhe-----SerValThr 152
DB 391 AGCTGTACCAATCCGAAAGCGATGTTCTGTGTGCTGTTTCTGTCGATTTATCGAT 450
QY 153 LeuAsnAlaGluThr-ProThrTrpAlaArgLeuMetAlaTrp-----AlaGlyIleVal 170
DB 451 GTCAACGCCAAACCCCGCGGTG-----CGTTCTTATCTGCGCTGACCTCGAGTG 507
QY 170 LeuAlaSerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaVal 190
DB 508 ATTAGCTTCTGTATATAGCTTTTGTATCTCTCGGCTCGTTTGTCCAGCTTACGTC 567
QY 190 GArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyVa 210
DB 568 -AAACCCGCAAGAGCTGGCTAAACTTGCACAGCGCTGATTGGTGTGGTTCGTCGG 626
QY 210 lPheAlaLeuArgLeu 215
DB 627 GTTCGCGCGCGCGCTG 642

RESULT 10
```

US-09-252-991A-15039
; Sequence 15039, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15039
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15039

Alignment Scores:
Pred. No.: 1,74e-18 Length: 681
Score: 221.00 Matches: 55
Percent Similarity: 50.00% Conservative: 46
Best Local Similarity: 27.23% Mismatches: 85
Query Match: 19.47% Indels: 16
DB: 4 Gaps: 6

US-09-459-573-10 (1-223) x US-09-252-991A-15039 (1-681)

```
QY 18 HieAlaValTyrLeuThrValGlyLeuPheValIleThr-----PhePhe 32
Db 58 TATCGAATCATGCTGGAACCTCGCTTCGTAGCCACCTCGCCACCTCGGCATGCTC 117
QY 33 AsnProGlyAlaAsnLeuPheValValGlnThrSerLeuAlaSerClyArgAla 52
Db 118 TCGCCGGCCGGACCTTCCTGATCATCCGCAACCGCGCGCGGTACCGCGCTCGCGG 177
QY 53 GlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeu 72
Db 178 GCGATGATGACCTCGCTGGGGGTGATTCTCGCGGTGGCCACCCACATGSCCTACTGCGTC 237
QY 73 PheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIleVal 92
Db 238 GCGCGCTGGCGGTGCTGATCACCACCGCCGCTGGCTGTTCAACGCGCTGAAGTACACC 297
QY 93 GlyGlyAlaTyrLeuLeuThrPheAlaTyrCysSerMetArgArgGlnSerThrProGln 112
Db 298 GCGCGGTCTACTGATCGGATCGCATCCAGCGCCCTGGCTCGCGCGCGCGC----- 351
QY 113 MetSerThrLeuGlnGlnProIleSer-----AlaProTyrTyrValPhe 127
Db 352 ---GGCACGCTCGACCTGGCGGTGCGCGGTGCGAGCGGTGCGCCACTGAGCGCGTTC 408
QY 128 PheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSer 147
Db 409 CTC---CAGGGTACTGTGCAACTGCTCAACCCCAAGGCCACGCTGTTCTCTCGCC 465
QY 148 IlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAla 167
Db 466 GTGTTCACCCAGGTGCTGAGCTGACTCC---AGCTTCGCGGAGAGCTCTGGTAGGCC 522
QY 168 GlyIleValLeuAla---SerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeu 186
Db 523 GGCATCATCGTGGCGCTCGCGCATCTGGTGGCGGTGCTGGTGGTGGTGGTGGTGGTGGT 582
QY 187 ProAlaValArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIleGlyAla 206
Db 583 GCGGTGGTGGCGCGGCTGGCGAGGCCCGAGGGGGTGGTGGCAAGCTGCTCGCGCGG 642
QY 207 IleIle 208
      :::::
```

Db 643 CTGCTG 648

RESULT 11
US-09-328-352-649
; Sequence 649, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 649
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-649

Alignment Scores:
Pred. No.: 1,8e-18 Length: 633
Score: 220.50 Matches: 54
Percent Similarity: 46.04% Conservative: 39
Best Local Similarity: 26.73% Mismatches: 106
Query Match: 19.43% Indels: 3
DB: 4 Gaps: 1

US-09-459-573-10 (1-223) x US-09-328-352-649 (1-633)

```
QY 16 ProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPheAsnProGly 35
Db 28 CCTCTTTTCAATTCGATGGCATTCGCTGGAGCAATA-----AGTCTGGG 78
QY 36 AlaAsnLeuPheValValGlnThrSerLeuAlaSerGlyArgAlaGlyValLeu 55
Db 79 CCAAGCTTTATTTATGATGGCAAAATTCATATATCAATATCACTAAATCAGTAAACATGCTTATTT 138
QY 56 ThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeu 75
Db 139 ACGCTTTAGAACCGGCACAGGTGCGCTCTTTTGGCTTTTATAGCGGTATGGGGTTA 198
QY 76 AlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIleValGlyGlyAla 95
Db 199 CAGCGACTTTTATTTGGCAGTGCCTTCAGCTTATCTAATTTTAAATAATGGTGGGCTG 258
QY 96 TyrLeuLeuThrPheAlaTyrCysSerMetArgArgGlnSerThrProGlnMetSerThr 115
Db 259 TATTTGCTTTGGCTTGTCTTTTAAATTTTAAACATGCCAAGAACCAATTGCTATGGAA 318
QY 116 LeuGlnGlnProIleSerAlaProTyrTyrValPhePheArgArgGlyLeuIleThrAsp 135
Db 319 AATGATGCCAAATCGAAGATGACTTATAAACAGCTACCGATATGTTGATTTACTCAG 378
QY 136 LeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAla 155
Db 379 TTAAGTAATCAAAATTTGCTGTGTACTAGCGAGTGTCTTACTGCTTTACTGCCAAAA 438
QY 156 GluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAlaSerIleIle 175
Db 439 GAATTTCCAAATTTATTTACTAGCTGCGCATTCACGCTCATTTGTTTATGATGACGGT 498
QY 176 TrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgAlaTyrGlyArg 195
Db 499 TGGTACTCATGTGTAGCAATGCTTTTATCTTCAGAGAACCTCGAAAAATGTTATTAANA 558
QY 196 MetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAlaLeuArgLeu 215
Db 559 GCAAAACCGGGTGTGACCGAGTGGCTGGAAGCATTTGTTAGTGTATTGGGCTTAAAGTTA 618
QY 216 IleTyr 217
      :::::
```

```
RESULT 12
US-09-328-352-4123
; Sequence 4123, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4123
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4123

Alignment Scores:
Pred. No.: 2,14e-18 Length: 708
Score: 220.50 Matches: 56
Percent Similarity: 43.26% Conservative: 37
Best Local Similarity: 26.05% Mismatches: 79
Query Match: 19.43% Indels: 43
DB: 4 Gaps: 6

US-09-459-573-10 (1-223) x US-09-328-352-4123 (1-708)
QY 7 LeuPheMetAspGluLeuThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeu 26
Db 55 ATAATATTAAAGATATTTCATGCTAGATCTCTCAAAATT---TTGGCATTGGATTA 111
QY 27 PheValIleThrPhe---PheAsnProGlyAlaAsnLeuPheValValGlnThrSer 45
Db 112 ATTGTCTGGCATGGTACTCACCCCTGGCCCAACATGATTTATCTCTCTCTCC 171
QY 46 LeuAlaSerGlyArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAla 65
Db 172 ATAGTCAGGGCAAAATCGCAGGATTTATCTCTCGGTGGCGTTGCGTTGTTGTA 231
QY 66 PheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuLeuThrGlnCysGluGluIle 85
Db 232 TTATCATGCTTGGCATCTTTCGGATTACAGCATTTGTTGTCAGTACCTTATGCA 291
QY 86 PheSerLeuIleArgIleValGlyGlyAlaTyrLeuLeuTyrPheAlaTyrCysSerMet 105
Db 292 TATGACACTATTCGATTTCGCGTCCGATGATCTTACTTTGTTAGCATGAAAGCTTTA 351
QY 106 ArgArgGlnSerThrProGlnMetSerThrLeuGlnGlnProIleSerAlaProTyr 125
Db 352 CGCCCAATGCCACCTATTTTAAATTAAGATTAGCGTTGACCTACCATTAAG 411
QY 126 ValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePhe 145
Db 412 TTATTTTAA---ATGGGCTTTTGACATTAATTAATTAATTAATTAATTAATTAATTA 468
QY 146 IleSerIlePhe----- 149
Db 469 TTATCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 528
QY 150 -----SerValThrLeuAsnAla----- 155
Db 529 CAATCGGGACTATACAAATTTTGTAAAGCTTTTCAAGTAATTCGCTGATTTGTTCT 588
QY 156 -----GluThrProThrTrpAlaArgLeuMetAlaTyr 166
Db 589 GCTGGTAGCATGCTCTTTTTCACAGAAACAAACCTTTGGCCAGCATTAACGCTGG 648
QY 167 Ala---GlyIleValLeuAlaSerIleIleTyrPheValPheLeu 180
Db 649 GTACATGGGAACAGTATTAGCCGGTCTTCGGTTTCTTCTTCTTA 693
```

```
RESULT 13
US-09-252-991A-9421
; Sequence 9421, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9421
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9421

Alignment Scores:
Pred. No.: 1.3e-16 Length: 783
Score: 207.00 Matches: 58
Percent Similarity: 48.57% Conservative: 44
Best Local Similarity: 27.62% Mismatches: 92
Query Match: 18.24% Indels: 16
DB: 4 Gaps: 5

US-09-459-573-10 (1-223) x US-09-252-991A-9421 (1-783)
QY 12 IleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhe 31
Db 136 GTACCATGATGAGAAATGCTGCTTCTGACCCCTGGCGGGGGTGTGGCATAGCCCTG 195
QY 32 PheAsnProGlyAlaAsnLeuPheValValGlnThrSerLeuAlaSerGlyArgArg 51
Db 196 GTACAGCCCGGTCCGATGTCGCCCTGGTGGTGGCGACCTCCCTGCACAGGCGCGCG 255
QY 52 AlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGly 71
Db 256 GCCGCGCTCGCAGCGCGCTGGCGCTGGCGGATTCCTCGCATACACCCCTGGTG 315
QY 72 LeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIle 91
Db 316 CTGACCGCGGTGCTGCTGCTGCTGACCCGTACGCCGTGCTGCTGCTGCTGCTGCTG 375
QY 92 ValGlyGlyValTyrLeuLeuTyrPheAlaTyrCysSerMetArg-----ArgGln 108
Db 376 CTCGGCGCGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
QY 109 SerThrProGlnMetSerThrLeuGln-----GlnProIleSerAlaPro 123
Db 436 GCGGACGCGCAGCGCGCGCTGACGCGGCGACCTGCCCGCTGCGCCCTG---GGGCCC 492
QY 124 TryptyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeu 143
Db 493 TGGCTG-----CGCGAGTGGCGACCAATCTGTTCATCCCAAGCGCTGCTG 540
QY 144 PhePheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeu 163
Db 541 TTATTCATCCCTGCTGCGGACGCTGATTCGCCGCGCAGATGCTGCTGCGCGCAACTG 600
QY 164 MetAlaTyrAlaGlyIleValLeuAlaSerIleIleTyrPheValPheLeuSerGlnAla 183
Db 601 GCGGTGCGCGCTGCTGCTGCGGATGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 184 PheSerLeuProAlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgVal 203
Db 661 CTTACCGCGCGCGCTGCGAG-----GCCGCGCTGTGGCGCGGTGCGCTGCTGCTG 711
QY 204 IleGlyAlaIleIleGlyValPheAlaLeu 213
```

```
Db 712 GACGCGCCTGCGGGTGGTGTCTCTGCTG 741
RESULT 14
US-09-252-991A-9478
; Sequence 9478, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9478
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9478
Alignment Scores:
Pred. No.: 4e-16 Length: 1596
Score: 207.00 Matches: 58
Percent Similarity: 48.57% Conservative: 44
Best Local Similarity: 27.62% Mismatches: 92
Query Match: 18.24% Indels: 16
DB: 4 Gaps: 5
US-09-459-573-10 (1-223) x US-09-252-991A-9478 (1-1596)
QY 12 IleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhe 31
Db 35 GTAGCCATGACGAAATGCTGTCTGTGACCTGGCGCGGTGTTCGCCATAGCCCTG 94
QY 32 PheAsnProGlyAlaAlaLeuPheValValGlnThrSerLeuAlaSerGlyArgArg 51
Db 95 GTCAGCCCCGTCCTCCGATGTCGCCCTGGTGTGGCAGCTCTCTGCACACGAGGGCGCG 154
QY 52 AlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGly 71
Db 155 GCGGCGCTGCCAGCGCGCTGGGCTGGCTGGCGATTCCTCTGCATACCACTGCTGTG 214
QY 72 LeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIle 91
Db 215 CTGACCGCGCTGCTGCTGTCTGACCGTACGCTGTCTGTTCGCATCTCGACGCG 274
QY 92 ValGlyGlyAlaTyrLeuLeuThrPheAlaTyrCysSerMetArg-----ArgGln 108
Db 275 CTCGCGCGCTGTACTGCGCTGGCTGGCGCTGGCGCTGGCGCTGGCTGGCTGGCGCGC 334
QY 109 SerThrProGlnMetSerThrLeuGln-----GlnProIleSerAlaPro 123
Db 335 GCGGACGCGCAGCGGCGCGCTCGACGGGGCACTGCCGCGCTGCCCTG-----GGGCCC 391
QY 124 TrpTyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeu 143
Db 392 TGGCTG-----CGCGAGTGGCGACCAATCTGTTCAATCCCAAGCGCTGTGTG 439
QY 144 PhePheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeu 163
Db 440 TTATTATCATGCTTGTCTGGCAGCCTGATTCGCCGCGCAGATGCTCGCTGGCGGCAACTG 499
QY 164 MetAlaTrpAlaGlyValLeuAlaSerIleThrArgValPheLeuSerClnAla 183
Db 500 GCGGTGGCGCGCTGCTGTGGCATTGGCGCTGCTGTGGCGCTGCTGTGGCGCTGCTG 559
QY 184 PheSerLeuProAlaValArgAlaTyrGlyArgMetGlnArgValAlaSerArgVal 203
Db 184 PheSerLeuProAlaValArgAlaTyrGlyArgMetGlnArgValAlaSerArgVal 203
Db 560 CTTACCGCGCGCGCTGCGAG-----GCCCGCCTGTTGCGCGCGGTGCCCTGGCTG 610
QY 204 IleGlyAlaIleIleGlyValPheAlaLeu 213
Db 611 GACGCGCGCTGCGGGTGGTGTCTCTGCTG 640
RESULT 15
US-09-252-991A-9352/G
; Sequence 9352, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9352
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9352
Alignment Scores:
Pred. No.: 4.22e-16 Length: 1650
Score: 207.00 Matches: 58
Percent Similarity: 48.57% Conservative: 44
Best Local Similarity: 27.62% Mismatches: 92
Query Match: 18.24% Indels: 16
DB: 4 Gaps: 5
US-09-459-573-10 (1-223) x US-09-252-991A-9352 (1-1650)
QY 12 IleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhe 31
Db 1586 GTAGCCATGACGAAATGCTGTCTGTGACCTGGCGCGGTGTTCGCCATAGCCCTG 1527
QY 32 PheAsnProGlyAlaAlaLeuPheValValGlnThrSerLeuAlaSerGlyArgArg 51
Db 1526 GTCAGCCCCGTCCTCCGATGTCGCCCTGGTGTGGCAGCTCTCTGCACACGAGGGCGCG 1467
QY 52 AlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGly 71
Db 1466 GCGGCGCTGCCAGCGCGCTGGGCTGGCTGGCGATTCCTCTGCATACCACTGCTGTG 1407
QY 72 LeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIle 91
Db 1406 CTGACCGCGCTGCTGCTGTCTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1347
QY 92 ValGlyGlyAlaTyrLeuLeuThrPheAlaTyrCysSerMetArg-----ArgGln 108
Db 1346 CTCGCGCGCTGTACTGCGCTGGCTGGCTGGCGCTGGCGCTGGCGCTGGCTGGCGCGC 1287
QY 109 SerThrProGlnMetSerThrLeuGln-----GlnProIleSerAlaPro 123
Db 1286 GCGGACGCGCAGCGGCGCGCTGCGCGGGCACTGCCGCGCTGCCCTG-----GGGCCC 1230
QY 124 TrpTyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeu 143
Db 1229 TGGCTG-----CGCGAGTGGCGACCAATCTGTTCAATCCCAAGCGCTGTGTG 1182
QY 144 PhePheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeu 163
Db 1181 TTATTATCATGCTTGTCTGGCAGCCTGATTCGCCGCGCAGATGCTCGCTGGCGGCAACTG 1122
QY 164 MetAlaTrpAlaGlyValLeuAlaSerIleThrArgValPheLeuSerGlnAla 183
Db 1121 GCGGTGGCGCGCTGCTGTGCGCATGGGCGCTGCTGTGCGCTGCTGTGCGCTGCTG 1062
```

us-09-459-573-10.rni

Wed Jan 26 08:14:34 2005

Qy 184 PheSerLeuProAlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgVal 203
Db ::: |||||:::
1061 CTTACCGCGCGCCCTGCAG-----GCCCGCTGTGTGCGCGGTGCCCTGCTG 1011
Qy 204 IleGlyAlaIleIleGlyValPheAlaLeu 213
Db ::: |||||:::
1010 GACGCGCCCTCGCGGTGTGTCTGCTG 981

Search completed: January 25, 2005, 13:41:53
Job time : 1364 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2005, 12:28:08 ; Search time 378 Seconds
(without alignments)
3389.770 Million cell updates/sec

Title:
Perfect score: 1135
Sequence: 1 MMQVHLFMDEITMDPLHAV.....IGAIQVFPALRIYEGVTQR 223

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09459573/runat_25012005_115349_28948/app_query.fasta_1.391
-DB=Published Applications NA -QWTF=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRANSHUMAN40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09459573 @CGN 1 1 354 @runat_25012005_115349_28948
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	225	19.8	1830121	14	US-10-329-960-1	Sequence 1, Appli
2	225	19.8	1830121	16	US-10-329-670-1	Sequence 1, Appli
3	225	19.8	1830121	18	US-10-158-865-1	Sequence 165, Appli
4	217	19.1	3309400	9	US-09-738-626-165	Sequence 1, Appli
5	217	19.1	3309400	9	US-09-738-626-1	Sequence 2918, Ap
6	175	15.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
7	175	15.6	9025608	15	US-10-156-761-1	Sequence 3368, Ap
8	168	14.8	32329	16	US-10-374-903A-1	Sequence 3747, Ap
9	168	14.8	32329	16	US-10-374-903A-1	Sequence 1, Appli
10	166	14.6	793	10	US-09-738-626-2570	Sequence 2570, Ap
11	166	14.6	793	10	US-09-738-626-2570	Sequence 13, Appli
12	166	14.6	793	10	US-10-494-672-295	Sequence 295, Appli
13	166	14.6	793	10	US-10-494-672-295	Sequence 1, Appli
14	166	14.6	793	10	US-10-494-672-295	Sequence 2570, Ap
15	164	14.4	2731718	17	US-10-329-670-1	Sequence 1, Appli
16	162	14.3	269223	16	US-10-282-122A-41840	Sequence 41840, A
17	146.5	12.9	621	16	US-10-156-761-246	Sequence 246, App
18	145	12.8	672	15	US-10-282-122A-30598	Sequence 30598, A
19	143	12.6	630	16	US-10-282-122A-30598	Sequence 30598, A
20	141.5	12.5	621	16	US-10-282-122A-30598	Sequence 30598, A
21	138.5	12.2	618	16	US-10-282-122A-30598	Sequence 30598, A
22	135	11.9	633	16	US-10-282-122A-30598	Sequence 30598, A
23	134.5	11.9	623	16	US-10-282-122A-30598	Sequence 30598, A
24	134	11.8	86941	16	US-10-282-122A-30598	Sequence 30598, A
25	133	11.7	85692	16	US-10-282-122A-30598	Sequence 30598, A
26	129.5	11.4	820	13	US-10-184-123-142	Sequence 142, App
27	127.5	11.2	627	16	US-10-282-122A-14918	Sequence 14918, A
28	126.5	11.1	1200	9	US-09-879-395-1	Sequence 1, Appli
29	126.5	11.1	1200	9	US-09-879-395-1	Sequence 1, Appli
30	125	11.0	618	16	US-10-184-123-142	Sequence 142, App
31	125	11.0	618	16	US-10-184-123-142	Sequence 142, App
32	124.5	10.9	630	16	US-10-282-122A-30598	Sequence 30598, A
33	123.5	10.9	630	16	US-10-282-122A-30598	Sequence 30598, A
34	114	10.0	609	15	US-09-738-626-165	Sequence 165, Appli
35	109	9.6	623	9	US-09-738-626-165	Sequence 165, Appli
36	108.5	9.6	630	15	US-10-282-122A-30598	Sequence 30598, A
37	104	9.2	9795	16	US-10-282-122A-30598	Sequence 30598, A
38	101.5	8.9	750	16	US-10-282-122A-30598	Sequence 30598, A
39	100.5	8.9	1893	16	US-10-282-122A-30598	Sequence 30598, A
40	100	8.8	543	16	US-10-282-122A-30598	Sequence 30598, A
41	96	8.5	633	16	US-10-282-122A-30598	Sequence 30598, A
42	95	8.4	636	16	US-10-282-122A-30598	Sequence 30598, A
43	93.5	8.2	1422	16	US-10-282-122A-30598	Sequence 30598, A
44	93	8.2	633	16	US-10-282-122A-30598	Sequence 30598, A
45	93	8.2	1234	16	US-10-425-114-20399	Sequence 20399, A

ALIGNMENTS

RESULT 1
US-10-329-960-1
; Sequence 1, Application US/10329960
; Publication No. US20030099277A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra
; FILE REFERENCE: P186P1
; CURRENT APPLICATION NUMBER: US/10329,960
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 1830121


```
/
/
/ NAME/KEY: misc feature
/ LOCATION: (140398)..(140398)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (142750)..(142750)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (145058)..(145058)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (145171)..(145171)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (145942)..(145942)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (147197)..(147197)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (150841)..(150841)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (152500)..(152500)
/ OTHER INFORMATION: n equals a, t, g or c
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (152530)..(152530)
/
/
/ Alignment Scores:
/ Pred No.: 6, 47e-13 Length: 1830121
/ Score: 225.00 Matches: 60
/ Percent Similarity: 44.78% Conservative: 43
/ Best Local Similarity: 26.09% Mismatches: 87
/ Query Match: 19.82% Indels: 40
/ DB: 14 Gaps: 4
/
/
/ US-09-459-573-10 (1-223) x US-10-329-960-1 (1-1830121)
/
/ QY 4 LeuValHisLeuPheMetAspGluThrMetAspProLeuHisAlaValTyrLeuThr 23
/ DB 1385069 ATGTGCAATTTATTT----- 1385083
/
/ QY 24 ValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGln 43
/ DB 1385084 ---GGATTA-----ATGACCCGAGGCCCTGATTTCTTTATGTAAGTCGA 1385125
/
/ QY 44 ThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGly 63
/ DB 1385126 ATGGCGGCAAGTAACCTTCGTCGTAACACATTTGGCGATTTAGGCATAACGCTTGC 1385185
/
/ QY 64 AspaAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu 83
/ DB 1385186 ATGCCCTTTTGGGGAATGCTTCTATGTTGGGATGCGCGTGTGTCGTTACCATTCCA 1385245
/
/ QY 84 GluIlePheSerLeuIleArgIleValGlyAlaTyrLeuTyrPheAlaTyrCys 103
/ DB 1385246 GCATTACATGGCGTTATATGTTGCTAGGTAGTATACATCTCTCGGTTTATTA 1385305
/
/ QY 104 SerMetArgGlnSerThrPro-----Gln 112
/ DB 1385306 ATGGCTCGCAATCAAAAAATACGCTAAATTCGACCTCTGATCTGAATTTAATCAA 1385365
/
/ QY 113 MetSerThrLeuGlnGlnProIleSerAlaProTyrValPhePheArgArgGlyLeu 132
/ DB 1385366 CAACCAACAATCAAAAAAATAATT-----TTGAAAGGCGCTT 1385401
```

```
133 IleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThr 152
1385402 TTAGTGAATTTATCCAAATGCAAAAGTCGTGCTGTTATTTTATAGTAGCTGATGCTGCTTC 1385461
/
/ QY 153 LeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAla 172
1385462 TTAGTAAATATCACTGAAATGTGGCAAATTTATCTGGCTTTTTCAGTGTATTGTGTAGAA 1385521
/
/ QY 173 SerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgAla 192
1385522 ACATTTGTTATTTTATGTGATTTTCATTTTTCAGTAAATATTCGCAAGCGTTTA 1385581
/
/ QY 193 TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAla 212
1385582 TACAGTCAATACAGCCGTTATATGATAATATGGCAGGTATGTTATTTTATTTTGGT 1385641
/
/ QY 213 LeuArgLeuIleTyrGluGlyValThrGln 222
1385642 TGTGTGCTTGTGTTATACGGCATCAACGAA 1385671
/
/
/ RESULT 2
/ US-10-329-670-1
/ ; Sequence 1, Application US/10329670
/ ; Publication No. US20040018503A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: Fleischmann et al.
/ ; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra-
/ ; TITLE OF INVENTION: Thereof, and Uses Thereof
/ ; FILE REFERENCE: FBI866P1
/ ; CURRENT APPLICATION NUMBER: US/10/329,670
/ ; PRIOR FILING DATE: 2002-12-24
/ ; PRIOR APPLICATION NUMBER: US 09/643,990
/ ; PRIOR FILING DATE: 2000-08-23
/ ; PRIOR APPLICATION NUMBER: US 08/487,429
/ ; PRIOR FILING DATE: 1995-06-07
/ ; PRIOR APPLICATION NUMBER: US 08/426,787
/ ; PRIOR FILING DATE: 1995-04-21
/ ; NUMBER OF SEQ ID NOS: 1
/ ; SOFTWARE: Patent in version 3.1
/ ; SEQ ID NO 1
/ ; LENGTH: 1830121
/ ; TYPE: DNA
/ ; ORGANISM: Haemophilus influenzae
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (4747)..(4747)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (9921)..(9921)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (10150)..(10150)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (29298)..(29298)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (36543)..(36543)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (36551)..(36551)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (36636)..(36636)
/ ; OTHER INFORMATION: n equals a, t, g or c
/ ;
/ ; FEATURE:
```

```

; NAME/KEY: misc_feature
; LOCATION: (40808)..(40810)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44416)..(44416)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44905)..(44905)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44975)..(44975)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45593)..(45593)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45732)..(45732)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (47036)..(47036)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51334)..(51334)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51602)..(51602)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51786)..(51786)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51805)..(51805)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55369)..(55369)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65309)..(65309)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65313)..(65313)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80024)..(80024)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (100091)..(100091)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (102696)..(102696)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (105121)..(105121)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature

```

```

; LOCATION: (107248)..(107248)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (117136)..(117136)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119750)..(119750)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119924)..(119924)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120038)..(120038)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (121344)..(121344)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122167)..(122167)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122336)..(122336)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131340)..(131340)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131360)..(131360)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (139910)..(139910)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (140398)..(140398)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142750)..(142750)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145058)..(145058)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145171)..(145171)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145942)..(145942)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (147197)..(147197)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (150841)..(150841)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (152500)..(152500)

```

us-09-459-573-10.rnpb

Wed Jan 26 08:14:34 2005

```

; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (152530)..(152530)

Alignment Scores:
Pred No.: 6,47e-13 Length: 1830121
Score: 225.00 Matches: 60
Percent Similarity: 44.78% Conservative: 43
Best Local Similarity: 26.09% Mismatches: 87
Query Match: 19.82% Indels: 40
DB: 16 Gaps: 4

US-09-459-573-10 (1-223) x US-10-329-670-1 (1-1830121)
Qy 4 LeuValHisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr 23
Db 1385069 ATTGTGCATTTATTT----- 1385083
Qy 24 ValGlyLeuPheValIleThrPhePheAenProGlyAlaAenLeuPheValValGln 43
Db 1385084 ---GGNTTA-----ATGAGCGCCAGGCGCTGATTTCTTTATGTAAGTCGA 1385125
Qy 44 ThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGlyValAlaLeuGly 63
Db 1385126 ATGGCGGCAGTAAGTCTCGTGTATACAGTTTGTGGCAATTTAGGCATAACGCTTGGC 1385185
Qy 64 AspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu 83
Db 1385186 ATCGGCTTTTGGGAATGCTTCTATGTTGGGATTTGGCGGTGTTTCGTTACCATTCGA 1385245
Qy 84 GluIlePheSerLeuIleArgIleValGlyGlyAlaTyrLeuLeuThrPheAlaTrpCys 103
Db 1385246 GCATTACATGGCGTTATATGTTGCTAGGTGGTAGTTACCTAGCATATCTCGGTTTTTTA 1385305
Qy 104 SerMetArgArgGlnSerThrPro-----Gln 112
Db 1385306 ATGGCTCGCAGTAAATAATACGCTAAATTTGAATCGCACTCTGACTGAAATTAATCAA 1385365
Qy 113 MetSerThrLeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgGlyLeu 132
Db 1385366 CAACCCACATCAAAAAGAAATTT-----TTGAAAGGCGTT 1385401
Qy 133 IleThrAspLeuSerAspProGlnThrValLeuPhePheIleSerIlePheSerValThr 152
Db 1385402 TTATGTAATTTATCAATGCAAAAGTCGTGGTATTTTAGTAGCGTGATGCGTTGTC 1385461
Qy 153 LeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAla 172
Db 1385462 TTATGTAATATCACTGAAATGTGGCAAAATTAATCTTGGCTTTTGGCAGTGATTTGGTAGAA 1385521
Qy 173 SerIleIleTrpArgValPheIleSerGlnAlaPheSerLeuProAlaValArgAla 192
Db 1385522 ACATTTGTTATTTTATGTCATTTTCATGTTTTCACGTAATATTGCGCAACGGTTTA 1385581
Qy 193 TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleGlyValPheAla 212
Db 1385582 TACAGTCATACAGCGTTATATGTAATATGCAATATGCGAGGTATGTTATTTTATTTTGGT 1385641
Qy 213 LeuArgLeuIleTyrGluGlyValThrGln 222
Db 1385642 TGTGTGCTTGTGTTATTAACGCAATCAACGAA 1385671

RESULT 3
US-10-158-865-1
; Sequence 1, Application US/10158865
; Publication No. US20040203093A1
; GENERAL INFORMATION:
; APPLICANT: Fletschmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P2C1D1
; CURRENT APPLICATION NUMBER: US/10/158,865
```


Qy 84 GluilePheSerLeuLeuAArgLeValGlyGlyAlaTyrlLeuLeuTrpPheAlaTrpCys 103
 Db 1385246 GCATTACATGCGGTATTATGTTGCTAGTGTAGTACTACATGCAATCTCGTGTITTTA 1385305
 Qy 104 SerMetArgGlnSerThrPro-----Gln 112
 Db 1385306 ATGGCTCCGCAATAAATAACGCTAAATTTGATTCGCACCTCTGATCTGAAATTTAATCAA 1385365
 Qy 113 MetSerThrLeuGlnGlnProIleSerAlaProTrpTyrlValPhePheArgGlyLeu 132
 Db 1385366 CAATCCACATCAAAAGAAATTT-----TTGAAGGGCTT 1385401
 Qy 133 IleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThr 152
 Db 1385402 TTAGTGAATTTATCCAAATGCAAAAGTCGGGTATTTTAGTACGATGATGCTGTGTC 1385461
 Qy 153 LeuAsnAlaGluThrProThrTrpAlaAArgLeuMetAlaTrpAlaGlyIleValLeuAla 172
 Db 1385462 TTAGTAAATATCACTGAAATGTGGCAATATCTTGGCTTTTGCATGATTTGGTAGAA 1385521
 Qy 173 SerIleIleTrpAArgValPheLeuSerGlnAlaPheSerLeuProAlaValAArgAla 192
 Db 1385522 ACATTTTGTATTTTATGTGATTTTCATTTGATTTTTCACGTAAATATGCGAAGCGTTTA 1385581
 Qy 193 TyrGlyArgMetGlnAArgValAlaSerAArgValIleGlyAlaIleIleGlyValPheAla 212
 Db 1385582 TACAGTCAATACAGCCGTATATTGATAATATGGCAGGTATTTGATTTTATTTTGTGT 1385641
 Qy 213 LeuArgLeuIleTyrlGlyValThrGln 222
 Db 1385642 TGTGTCTTGTATTATTAACGGCATCAACGAA 1385671

RESULT 4

US-09-738-626-165
 ; Sequence 165, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 165
 ; LENGTH: 678
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum

US-09-738-626-165

Alignment Scores:
 Pred. No.: 6,68e-17 Length: 678
 Score: 217.00 Matches: 63
 Percent Similarity: 50.45% Conservative: 48
 Best Local Similarity: 28.64% Mismatches: 81
 Query Match: 19.12% Indels: 28
 Gaps: 9
 Db:

US-09-459-573-10 (1-223) x US-09-738-626-165 (1-678)
 Qy 19 AlaValTyrlLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu 38
 Db 22 GCGCTTTTCTG-----GTGTGATCGCAGCAATTTGCAATCCCTGGGCGACACCTT 72
 Qy 39 PheValValValGlnThrSerLeuAlaSerGlyAArgAlaGlyValLeuThrGlyLeu 58
 Db 73 TTCCAGATCATCAGGCTAAGT---GCCAAAACCGCGGTGATGGCGTACTGACTGCCGTA 129
 Qy 59 GlyValAlaLeuGlyAspAlaPheTyrlSerGlyLeuGlyLeuPheGlyLeuAlaThrLeu 78
 Db 130 GGCATCATGGTGGGAACTCCATCTGGATCATAGCAGCTCTCTTGGGCTCTCGGCACTG 189
 Qy 79 IleThrGlnCysGluGluIlePheSerLeuIleAArgIleValGlyGlyAlaTyrlLeu 98
 Db 190 ATCTCCAGTATCCAGCAATTTTGAACCTGTTGCAGCTCGTGGTGGCGGTATTGAC 249
 Qy 99 TrpPheAlaTrpCysSerMetAig-----ArgGlnSerThrProGlnMetSer 114
 Db 250 TGGATGGGCATCGGGCGGTGAGGTCAATGTTGACGAAACGCTCCACACAGCAAGCTGCA 309
 Qy 115 ThrLeuGlnGlnProIle-----SerAlaProTrp 124
 Db 310 GCGGATTTCAAGCTGTAGAGAAATACGTTGGTGACAGCGCGCTGCATCTGCGGAGTG 369
 Qy 125 TyrValPhePheAArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhe 144
 Db 370 TGCCAGCTATTGATCTGGCATTTGCTACCACTTGTCCAAACCCCAAGCTGTGCTGTTT 429
 Qy 145 PheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaAArgLeuMet 164
 Db 430 TTTGGTTCGTTTTGGCCCAATTTTGTAGACCTGACATGGGAATCGGCTGGAGTATTTC 489
 Qy 165 AlaTrpAlaGlyIleValLeuAlaSerIleIleTrpAArgValPheLeuSerGlnAlaPhe 184
 Db 490 ATTGGAGTCTTCTCACCCTCCTGCGCTGCTGTGTTTGTG-----GGTTTC 537
 Qy 185 SerLeuProAlaValAArgAlaTyrlGlyAArgMetGlnAArgValAlaSerAArgValIle 204
 Db 538 CCGGTCTTGGTCGGCAAACTAGCGCTGGCTCACCAGAAATGGAGCC-----ATCATC 591
 Qy 205 GlyAlaIleIleGlyValPheAlaLeuArgLeu-----IleTyrlGlyGlyVal 220
 Db 592 GACCTGCTAACGGGGGTGATTTTCATCGGCTGGGAATGTTTCATGATCTTCGAGGGGTT 651

RESULT 5

US-09-738-626-1
 ; Sequence 1, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0


```
Db 4201790 ATCGTGAAGTACGCGGGCGGGGTATCTGACCTGGCTCGGTTGGCGATGTCGGGGC 4201731
Qy 107 -----ArgGlnSerThrProGlnMetSerThrLeuGlnGlnProIleSer 121
Db 4201730 GCGTGGGAGATGTCGCGGACCGCGCGGGACCGCGCGGCGACCGCTCGCG 4201671
Qy 122 -----AlaProTrpTyrrValPhePheArgGlyLeuIleThrAspLeu 136
Db 4201670 CCGGTCCGCGAGAGCGGCC-----TTCGGGGGGGTTGCTGCTCAGCCCTC 4201623
Qy 137 SerAsnProGlnThrValLeuPhePheIleSerIlePhe-----SerValThrLeuAsn 154
Db 4201622 TTCAACCGAAGCGGATCTCTGCTGCTGCTCTTCGTCGCTTCTTCGTCGACCGGG 4201563
Qy 155 AlaGluThrProThrTrpAlaGluLeuMetAlaTrpAlaGlyLeuValLeuAlaSerIle 174
Db 4201562 TAGCCCTACCGCGGCTGCTCTGCTGCTGCTCGGCGCTTCGCCAGCTGGCGAGCTTC 4201503
Qy 175 IleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgArgAlaTrpGly 194
Db 4201502 CTGTACTCTACCGCGGTG-----ATCTTCAGCGGCACGAAAGCTGGCGCGCTTCCGC 4201449
Qy 195 ArgMetGlnArgVal-----AlaSerArgValIleGlyAlaIleIleGlyValPhe 211
Db 4201448 CGACGCAAGCGGCTCTCCGCGGGGCGCACGACCGCGCGGCGGCGCTCTCTCTGGGCTTC 4201389
Qy 212 AlaLeuLeuIleGlyLeuGluGly 219
Db 4201388 GCGGTGAGCTGACACTGGCGCGC 4201365
```

RESULT 9

```
US-10-156-761-3368
; Sequence 3368, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3368
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(651)
US-10-156-761-3368
```

```
Alignment Scores:
Pred. No.: 1,038-11 Length: 651
Score: 175.00 Matches: 60
Percent Similarity: 43.72% Conservative: 34
Best Local Similarity: 27.91% Mismatches: 97
Query Match: 15.42% Indels: 24
DB: Gaps: 8
```

US-09-459-573-10 (1-223) x US-10-156-761-3368 (1-651)

```
Qy 21 TyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheVal 40
|||||
|||||
|||||
|||||
```

```
Db 28 TACCTC---GCAGGCGTTTCTCTGATCTGCTCTGCTC---CCGCGTCCGAACTCGCTGTAC 81
Qy 41 ValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeuGlyVal 60
Db 82 GTGTTGTCGCTCGCGCGCGCGCAAGGCGGTACGCGCGCGATACACGCGAGCCGCGGCGTC 141
Qy 61 AlaLeuGlyAspAlaPheTyrrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThr 80
Db 142 TGGTCCGGTGAACCCGCTGATGACGCTGTCGCGCGCGGAGTCCCTCGCTGTCTCCAG 201
Qy 81 GlnCysGluGluIlePheSerLeuIleArgIleValGlyGlyAlaTyrrLeuLeuTrpPhe 100
Db 202 GCGAACGCGCTGCTGTCGGGATCTGAAGTACGCGCGCGCGGCGGTATCTGACCTGGCTC 261
Qy 101 AlaTrpCysSerMetArg-----ArgGlnSerThrProGlnMetSer 114
Db 262 GCGTTTCGCGATGCTGCGCGCGCGCTGGGAGATGTGGCGGACCCGCGCGGACCGCGCGGAC 321
Qy 115 ThrLeuGlnGlnProIleSer-----AlaProTrpTyrrValPhePheArg 129
Db 322 GCGGCGCGCGGACCGCTGCGCGCGGTGCGCGGAGCGGCGC-----TTCGG 369
Qy 130 ArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePhe 149
Db 370 CGGCGTTCGTCGTCAGCTCTTCAACCGAAGCGGATCTCTGCTCTGTCGCTCTTC 429
Qy 150 -----SerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAla 167
Db 430 GTTCAGTTCGTCGACCGCGGTACGCTTACCGCGCGCTCTCTGCTCTGCTCTCGCGCGC 489
Qy 168 GlyIleValLeuAlaSerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuPro 187
Db 490 TTCGCCAGCTGGCGGACTCTCTGACTCTACCGCGGTG-----ATCTTCAGCGGCGACG 543
Qy 188 AlaValArgAlaTyrrGlyArgMetGlnArgVal-----AlaSerArgValIle 204
Db 544 AAGCTGGCGCGCGCTTCCGCGCGACGCAAGCGGCTCTCCGCGGGGCGCACGACCGCGCG 603
Qy 205 GlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyrrGluGly 219
Db 604 GCGCGCTCTTCTGCGGCTTCGCGCGTGAAGCTGACACTGCGCGCGC 648
```

RESULT 10

```
US-10-156-761-3747
; Sequence 3747, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3747
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(615)
US-10-156-761-3747
```

Alignment Scores:

Pred. No.:	6,980-11	Length:	615
Score:	168.00	Matches:	52
Percent Similarity:	45.27%	Conservative:	39
Best Local Similarity:	25.8%	Mismatches:	90
Query Match:	14.80%	Indels:	20
DB:	15	Gaps:	8

US-09-459-573-10 (1-223) x US-10-156-761-3747 (1-615)

19	AlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu	38
19	GCGCCCTCTCGCATGATCTCTCTCGTG-----TTCACGCCCGGCGCGAGCTGG	72
39	PheValValValGlnThrSerLeuAlaSerGlyArgAlaGlyValLeuThrGlyLeu	58
73	GCCTACCGCATCGCGCGGAGCTCGGGAC-----CGTTCTGCTGCTCCCGCGGTGGCC	126
59	GlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyValLeuThrLeu	78
127	GGGCTGTGGCGGATACCGCGGGTACACCTCTCGCGTGGCGCGCTGTGGTGGTATC	186
79	IleThrGlnCysGluGluIlePheSerLeuIleArgIleValGlyGlyAlaTyrLeuLeu	98
187	GTCCCGCGCTCCCGAGCCGTGCTACCGCTCTACCGTCTCTGGGGCGCGCTACCTGAT	246
99	TrpPheAlaTrpCysSerMetArgGlnSerThrProGlnMetSerThrLeuGlnGln	118
247	TGGTCTCGGCTGGAGCGTTCTGGCGCGCGCGCACATCCCAGGCGCTCGCG-----GAGCGC	303
119	ProIleSerAlaProTrpTyrValPhePheArgGlyLeuIleThrAspLeuSerAsn	138
304	GTGGCGGCTTCCAGGTGGCGGATCTGTGTGAGGGGCGCGGGATCAGCGGCTG-----AAC	360
139	ProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsn-----	154
361	CCCAAGGCGTGTGTGTACTTCTCTGTCTCCCGCAGTTTCATCCACCCGCGTGAAGGG	420
155	-----AlaGlnThrProThrTrpAlaArgLeu---MetAlaTrpAlaGlyIle	169
421	TGGCCCGTAGCGGCTCAGACCGGTCTGTTCGGCACGCTCCACATGGCAGCTGCGCGCTG	480
170	Val-----LeuAlaSerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuPro	187
481	GTCTACCTGGCGGTGGCGGCTTGGCCCGCGCACCGTACTGAAG-----GCCCGCGCCG	531
188	AlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIle	207
532	ACGGCGGCTCGCGCGGTGGCGCGAGTTCAGCGCGAACCATGATGATCTCATCGCGGGTTC	591
208	Ile	208
592	CTC	594

RESULT 11

```

US2004-374-903A-1
; Sequence 1, Application US/10374903A
; Publication No. US20040038250A1
; GENERAL INFORMATION:
; APPLICANT: University of Oviedo
; APPLICANT: Astur Pharma, S.A.
; TITLE OF INVENTION: The gene cluster for thienamycin biosynthesis,
; FILE OF INVENTION: genetic manipulation and utility
; FILE REFERENCE: Thienamycin-UO-AP
; CURRENT APPLICATION NUMBER: US/10/374,903A
; CURRENT FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 32329
; TYPE: DNA
; ORGANISM: Streptomyces cattleya
; PUBLICATION INFORMATION:
; AUTHORS: Nunez, Luz Elena
; AUTHORS: Mendez, Carmen

```

```
; Sequence 2570, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2570
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2570

Alignment Scores:
Pred. No.: 1,4e-10 Length: 669
Score: 166.00 Matches: 57
Percent Similarity: 49.31% Conservative: 50
Best Local Similarity: 26.27% Mismatches: 80
Query Match: 14.63% Indels: 30
DB: 9 Gaps: 8

US-09-459-573-10 (1-223) x US-09-738-626-2570 (1-669)
QY 26 LeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGlnThrSer 45
Db CTCAATTGGTGGCGAGTTATCCCGGGCGCTGATACCTTTTCTCTCTCGC----- 87
QY 46 LeuAlaSerGlyArgAlaGlyValLeuThrGlyLeu---GlyValAlaLeuGlyAsp 64
Db TTAGCCACCGCTCCAGAGCGCAGCGATCGCTGGGTCGCCGCGATCGTCACCGGACTC 147
QY 65 AlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu 84
Db ACGGTGTGGGTGACGCTGACGCTGCTGGGAGCAGCGCGCTGCTCACCACCTATCCGTCG 207
QY 85 IlePheSerIleAlaGlyValGlyAlaTyrLeuLeuThrPheAlaTrpCysSer 104
Db ATTCGCGATCATCGATCTGCGCGCAGCTACCTAAGCTTCATTGGGTACAAGTTG 267
QY 105 MetArgArgGlnSerThrProGlnMetSerThrLeuGln----- 117
Db CTGCGCTCGCGCTCGAGAGAGCTTATCGACGCCCGCCAGTTCCGTTTCAACGCCGATGCC 327
QY 118 GlnProIleSerAlaProTrpTrpVal-----PhePheArg 129
Db CCACTATC-----CCGATCGGTGAGAACGACTGGGACCCGCACTCAGGTATATCGA 381
QY 130 ArgGlyLeuIleThrAspSerAsnProGlnThrValLeuPhePheIleSerIlePhe 149
Db CAAGGTTGGCCACCACTGTCACACCTCAAGTTGTGATGACTTCCGCGCAATTCG 441
QY 150 SerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGly 169
Db GTCCTGTGATGCCAGCGCACCCCA-----TCACCGGTGCTGGCGTCTCTCT 486

; Sequence 13, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; APPLICANT: Kim, Jun-Won
; APPLICANT: Lee, Heung-Schick
; APPLICANT: Hwang, Byung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CP2
; CURRENT APPLICATION NUMBER: US/09746,660A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/606740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 13
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(769)
; OTHER INFORMATION: RXC02390
US-09-746-660A-13

Alignment Scores:
Pred. No.: 1,78e-10 Length: 792
Score: 166.00 Matches: 57
Percent Similarity: 49.31% Conservative: 50
Best Local Similarity: 26.27% Mismatches: 80
Query Match: 14.63% Indels: 30
DB: 10 Gaps: 8

US-09-459-573-10 (1-223) x US-09-746-660A-13 (1-792)
QY 26 LeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGlnThrSer 45
Db CTCAATTGGTGGCGAGTTATCCCGGGCGCTGATACCTTTTCTCTCTCGC----- 187
QY 46 LeuAlaSerGlyArgAlaGlyValLeuThrGlyLeu---GlyValAlaLeuGlyAsp 64
Db TTAGCCACCGCTCCAGAGCGCAGCGATCGCTGGGTCGCCGCGATCGTCACCGGACTC 247
```


Alignment Scores:

Pred. No.: 4.3e-05 Length: 2731748
Score: 164.00 Matches: 45
Percent Similarity: 52.70% Conservative: 33
Best Local Similarity: 30.41% Mismatches: 56
Query Match: 14.45% Indels: 14
DB: 17 Gaps: 4

US-09-459-573-10 (1-223) x US-10-297-465A-1 (1-2731748)

```
QY      6 HisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyr---LeuThrVal 24
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621056 CACTTCTTGCAGAGAACGCGCATGCTCTCTATTATTTCATCTGACCGTG 2621115
      |||      |||      |||      |||      |||      |||      |||      |||
QY      25 GlyLeuPheValIleThrPhePheAnProGlyAlaAsnLeuPheValValGlnThr 44
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621116 CTGATGTTTAGCATC-----AGTCCGGGGCCAGCCATGATGTTGTGCTTCAGCAA 2621166
      |||      |||      |||      |||      |||      |||      |||      |||
QY      45 SerLeuAlaSerGlyArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAsp 64
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621167 TCCAGAGAACGGGGTAAACTGGTCTGGCTGCAGTGTCTGGGACTGAGATTGGCGTA 2621226
      |||      |||      |||      |||      |||      |||      |||      |||
QY      65 AlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGlu 84
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621227 TTTATTACGTATCCTCACCGCATTTGGGTATCAGTACTGTTTAAAGAAATACCCATCC 2621286
      |||      |||      |||      |||      |||      |||      |||      |||
QY      85 IlePheSerLeuIleArgIleValGlyGlyAlaTyrLeuLeuTrpPheAlaTrpCysSer 104
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621287 ATTTATACCGGCTGCAAGGATAGGTGGCGCTATCTGCTTTACATCGCCTACCTCAGC 2621346
      |||      |||      |||      |||      |||      |||      |||      |||
QY      105 MetArgArgGlnSer-----ThrProGlnMetSerThrLeuGlnGlnProIle 120
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621347 TGGCCCCGTGAGAATGCTTCAAAACACAGACTCTCTACAGCGTCC----- 2621388
      |||      |||      |||      |||      |||      |||      |||      |||
QY      121 SerAlaProTrpTyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGln 140
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621389 CGTTCAAGTTACACAGGCACCTTCATACAAGGAGTGCTGATTAACTGACGAATCCCAAG 2621448
      |||      |||      |||      |||      |||      |||      |||      |||
QY      141 ThrValLeuPhePheIleSerIle 148
      |||      |||      |||      |||      |||      |||      |||      |||
Db 2621449 ATCGTTTGTGTTCTTCCTCAGTCTG 2621472
```

Search completed: January 25, 2005, 15:26:48
Job time : 5150 secs